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US-09-524-100C-6 Sequence 6, Appli US-10-212-507-6 Sequence 6, Appli US-08-171-382-4 Sequence 4, Appli US-08-309-420-4 Sequence 4, Appli US-08-309-419-4 Sequence 4, Appli	US-09-294-531B-30 Sequence 30, Appl PCT-US5-11856-4 Sequence 4, Appli	PCT-US95-11878-4 Sequence 4, Applı US-09-252-991A-18381 Sequence 18381, A	US-09-902-540-16488 Sequence 16488, A US-09-328-352-7471 Sequence 7471, Ap	US-09-252-991A-30247 Sequence 30247, A	US-08-306-063-50 Sequence 50, Appl	US-08-833-485-50 Sequence 50, Appl US-09-137-440-50 Sequence 50, Appl	US-09-252-991A-19480 Sequence 19480, A	US-09-252-991A-33090 Sequence 33090, A	US-09-252-991A-26815 Sequence 26815, A	US-09-248-796A-15217 Sequence 15217, A	US-09-036-98/A-16 Sequence 18, Appl	US-09-603-207-18 Sequence 18, Appl	US-09-252-991A-19381 Sequence 19381, A	US-09-540-236-20/0 Sequence 20/0, Ap US-08-759-581B-22 Sequence 22, Appl	US-09-304-711-22 Sequence 22, Appl	US-09-173-281-22 Sequence 22, Appl	US-09-270-767-45388 Sequence 45386, A	US-09-252-991A-27479 Sequence 27479, A	US-09-270-767-60926 Sequence 60926, A	US-09-252-991A-29589 Sequence 29589, A	US-09-252-991A-32437 Sequence 32437, A	US-09-198-4924-903 Sequence 903, App US-09-438-185A-842 Sequence 842, App	US-09-252-991A-25490 Sequence 25490, A	US-09-3/9-230-8 US-09-934-899-10 Sequence	US-09-252-991A-17011 Sequence	US-09-543-681A-7085 sequence IIS-09-934-868-30 Sequence	US-08-222-619-5 Sequence	US-09-252-991A-29391 sequence US-09-949-016-5963 Sequence	US-09-949-016-11630 Sequence	PCT-US95-04075-5 Sequence US-09-252-991A-30304 Sequence	US-09-252-991A-25191 Sequence	US-09-489-039A-8415 Sequence 8415, Ap	US-09-25Z-991A-3Z5/3 Sequence 3Z5/3, A US-08-36Z-512A-2 Sequence 2, Appli	US-08-964-939-2 Sequence 2, Appli	US-09-540-236-2761 Sequence 2761, Ap US-09-854-774-2 Sequence 2, Appli	US-09-902-540-11019 Sequence 11019, A	US-09-667:135-30 Sequence 30, Appl 119-09-567:135-30 Sequence 27833, A	US-09-252-331A-2/833 Sequence 28, Appl	US-09-252-991A-16991 Sequence 16991, A	US-10-053-510-19 Sequence 19, Appl	US-09-107-532A-6115 Sequence 0115, Ap	US-09-511-719-2 Sequence	US-09-685-166A-895 Sequence	US-09-879-792-14 Sequence 14, Appl	US-09-8/9-8/9-895 Sequence 895, App	US-09-759-143-932 Sequence 932, App	US-08-362-512A-4 Sequence 4, Appli
4 US-09-524-100C-6 Sequence 6, Appli 4 US-10-212-507-6 Sequence 6, Appli 1 US-08-309-420-4 Sequence 4, Appli 1 US-08-309-419-4 Sequence 4, Appli 1 US-08-309-419-4 Sequence 4, Appli	3 US-09-294-531B-30 Sequence 30, Appl Sequence 4, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6	5 PCT-US95-11878-4 Sequence 4, Appl1 4 US-09-252-991A-18381 Sequence 18381, A	4 US-09-902-540-16488 Sequence 16488, A 4 US-09-328-352-7471 Sequence 7471, Ap	4 US-09-252-991A-30247 Sequence 30247, A	60 1 US-08-306-063-50 Sequence 50, Appl	60 1 US-08-833-485-50 Sequence 50, Appl 60 3 US-09-137-440-50 Sequence 50, Appl	60 4 US-09-252-991A-19480 Sequence 19480, A	60 4 US-09-252-991A-33090 Sequence 33090, A	61 4 US-09-252-991A-26815 Sequence 26815, A	61 4 US-09-248-796A-15217 Sequence 15217, A	62 3 US-09-370-700-18 Sequence 18, Appl	62 4 US-09-603-207-18 Sequence 18, Appl	63 4 US-09-252-991A-19381 Sequence 19381, A	64 2 US-08-759-581B-22 Sequence 22, Appl	64 3 US-09-304-711-22 Sequence 22, Appl	64 4 US-09-173-281-22 Sequence 22, Appl	64 4 US-09-270-767-45388 Sequence 45386, A 65 4 HG-09-634-238-411 Semience 411. Add	66 4 US-09-252-991A-27479 Sequence 27479, A	66 4 US-09-270-767-60926 Sequence 60926, A	68 4 US-09-252-991A-29589 Sequence 29589, A	68 4 US-09-252-991A-32437 Sequence 32437, A	68 4 US-09-196-4324-905 Sequence 942, App	69 4 US-09-252-991A-25490 Sequence 25490, A	72 4 US-09-914-899-10 Sequence	72 4 US-09-252-991A-17011 Sequence	72 4 US-09-543-681A-7085 sequence 72 4 US-09-934-868-30 Sequence	74 1 US-08-222-619-5 Sequence	74 4 US-09-252-991A-29391 Sequence	74 4 US-09-949-016-11630 Sequence	74 5 PCT-US95-04075-5 Sequence 76 4 US-09-252-991A-30304 Sequence	4 US-09-252-991A-25191 Sequence	4 US-09-489-039A-8415 Sequence 8415, Ap	4 US-09-252-991A-323/3 Sequence 323/3, A 1 US-08-362-512A-2 Sequence 2, Appli	3 US-08-964-939-2 Sequence 2, Appli	4 US-09-540-236-2761 Sequence 2/61, Ap 4 US-09-854-774-2 Sequence 2, Appli	4 US-09-902-540-11019 Sequence 11019, A	4 US-09-667-135-30 Sequence 30, Appl 4 HS-09-252-9912-27833 Sequence 27833, A	4 US-09-667-135-28 Sequence 28, Appl	4 US-09-252-991A-16991 Sequence 16991, A	4 US-10-053-510-19 Sequence 19, Appl	4 US-09-107-532A-6115 Sequence 5115, Ap	4 US-09-691-840-2 Sequence	4 US-09-685-166A-895 Sequence	4 US-09-879-792-14 Sequence 14, Appl	4 US-09-6/9-426-695 Sequence 895, App	4 US-09-759-143-932 Sequence 932, App	1 US-08-362-512A-4 Sequence 4, Appli
US-09-524-100C-6 Sequence 6, Appli US-10-212-507-6 Sequence 6, Appli US-08-171-382-4 Sequence 4, Appli US-08-309-420-4 Sequence 4, Appli US-08-309-419-4 Sequence 4, Appli	6 454 3 US-09-294-531B-30 Sequence 30, Appl 6 454 5 PCT-US5-11856-4 Sequence 4, Appli	6 454 5 PCT-US95-11878-4 Sequence 4, Applı 6 455 4 US-09-252-991A-18381 Sequence 18381, A	6 455 4 US-09-902-540-16488 Sequence 16488, A 6 457 4 US-09-328-352-7471 Sequence 7471, Ap	6 458 4 US-09-252-991A-30247 Sequence 30247, A	6 460 1 US-08-306-063-50 Sequence 50, Appl	6 460 1 US-08-833-485-50 sequence 50, Appl 6 460 3 US-09-137-440-50 Sequence 50, Appl	6 460 4 US-09-252-991A-19480 Sequence 19480, A	6 460 4 US-09-252-991A-33090 Sequence 33090, A	6 461 4 US-09-252-991A-26815 Sequence 26815, A	6 461 4 US-09-248-796A-15217 Sequence 15217, A	6 462 3 US-09-370-700-18 Sequence 18, Appl	6 462 4 US-09-603-207-18 Sequence 18, Appl	.6 463 4 US-09-252-991A-19381 Sequence 19381, A	.6 464 2 US-09-340-236-20/0 Sequence 20/0, Ap. 6 464 2 US-08-759-581B-22 Sequence 22, Appl	6 464 3 US-09-304-711-22 Sequence 22, Appl	.6 464 4 US-09-173-281-22 Sequence 22, Appl	6 464 4 US-09-270-767-45388 Sequence 45388, A	6 466 4 US-09-252-991A-27479 Sequence 27479, A	.6 466 4 US-09-270-767-60926 Sequence 60926, A	.6 468 4 US-09-252-991A-29589 Sequence 29589, A	.6 468 4 US-09-252-991A-32437 Sequence 32437, A	6 468 4 US-US-198-4324-903 Sequence 942, App	6 469 4 US-09-252-991A-25490 Sequence 25490, A	.6 472 4 US-09-34-899-10 Sequence	.6 472 4 US-09-252-991A-17011 Sequence	.6 472 4 US-09-543-681A-7085 sequence 6 472 4 HS-09-934-868-30 Sequence	.6 474 1 US-08-222-619-5 Sequence	.6 474 4 US-09-252-991A-29391 sequence 6 474 4 HS-09-949-016-5963 Sequence	.6 474 4 US-09-949-016-11630 Sequence	.6 474 5 PCT-US95-04075-5 Sequence	.6 478 4 US-09-252-991A-25191 Sequence	.6 481 4 US-09-489-039A-8415 Sequence 8415, Ap	.6 482 4 US-US-252-991A-323/3 Sequence 323/3, A .6 485 1 US-08-362-512A-2 Sequence 2, Appli	.6 485 3 US-08-964-939-2 Sequence 2, Appli	.6 485 4 US-U9-540-236-2761 Sequence 2701, Ap .6 485 4 US-09-854-774-2 Sequence 2, Appli	.6 485 4 US-09-902-540-11019 Sequence 11019, A	.6 489 4 US-09-667-135-30 Sequence 30, Appl	.6 490 4 US-09-667-135-28 Sequence 28, Appl	.6 490 4 US-09-252-991A-16991 Sequence 16991, A	.6 490 4 US-10-053-510-19 Sequence 19, Appl	.6 491 4 US-09-107-532A-6115 Sequence blls, Ap	.6 492 4 US-09-691-840-2 Sequence	.6 492 4 US-09-685-166A-895 Sequence	492 4 US-09-879-792-14 Sequence 14, Appl	492 4 US-09-079-143-895 Sequence 895, App	492 4 US-09-759-143-932 Sequence 932, App	491 1 HS-08-162-512A-4 Sequence 4, Appli

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Sequence 4490, Ap
Sequence 5, Appli
Sequence 3717, Ap
Sequence 15, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 134, Ap
Sequence 12373, A
Sequence 12373, A
Sequence 12373, A
Sequence 9830, A
Sequence 9830, A
Sequence 9830, A
Sequence 25133, A
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24, Appl
17, Appl
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US-09-370-368-9
US-09-252-991A-19476
US-09-253-681A-4490
US-09-023-587A-6
US-09-438-185A-748
US-09-438-185A-748
US-09-544-683-2
US-10-192-419-2
US-09-544-683-2
US-09-544-683-2
US-09-544-683-2
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US-09-544-683-3
US-09-252-991A-19909
US-09-252-991A-19909
US-09-902-540-10128
US-09-902-540-10128
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US-09-902-540-14945
US-08-793-229-34
US-09-285-957-34
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Patent No. 6730480

GENERAL INFORMATION, STUART M

APPLICANT: Brian, WATTENBERG W

APPLICANT: Brichard J. ANDREA J

TITLE OF INVENITION: SPHINGOSINE KINASE ENZYME

FILE REFERENCE: PITSON=1

CURRENT APPLICATION NUMBER: US/09/959,897

CURRENT FILING DATE: 2001-11-13

PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: AU PQ 0339

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 56

SOFTWARE: PATENTIN VERSION 3.1
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ORGANISM: Homo sapiens
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RESULT 2
US-09-970-516-2
Sequence 2, Application US/09970516
Factor No. 6610534
GENERAL INFORMATION:
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
                              181 SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                      241 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVWHLFYVRAGVSRAMLL 300
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SEKYRRLGEMRFTLGTFILRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
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87.5%; Score 336; DB 4; Length 384;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 336; Conservative 0; Mismatches 0; Indels
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US-10-053-510-21
; Sequence 21, Application US/10053510
; Patent No. 6830881
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyrst, Henrik
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LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Human
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US-09-949-016-7026
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Sequence 9811, Application US/09949016

Sequence 9811, Application US/09949016

GENERAL INFORMATION:

APPLICANT: URNER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 00/241, 755

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR APPLICATION WUMBER: 60/231, 498

PRIOR APPLICATION NUMBER: 60/231, 498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

WUMBER OF SEQ ID NOS: 207012

SOFTWARE: Pasted for Windows Version 4.0

SEQ ID NO 9811
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TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES, TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 200116.4020.

CURRENT APPLICATION NUMBER: US/10/053,510

CURRENT FILING DATE: 2002-01-17

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 2: LENGTH: 368
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                                                                                                                                                                                                                                                Query Match

83.3%; Score 320; DB 4; Length 368;
Best Local Similarity 100.0%; Pred. No. 3.2e-303;
Matches 320; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 9.5e-249;
iive 0; Mismatches 0;
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US-09-949-016-9811
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73 DALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNE 132

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FAREMAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7026
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                                                                                              1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
1 DALVUMSGDGLMHEVUNGLMERPDWETAIOKPLCSLPAGSGNALAASLMHYAGYEQVTNB
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                                                                                                                                                                                      253 PDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHM
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100.0%; Pred. No. 4.9e-235;
tive 0; Mismatches 0;
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US-09-796-487-3
; Sequence 3, Application US/09796487
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Best Local Similarity 100.
Matches 250; Conservative
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TLING DATE: 1998-12-04
APPLICATION NUMBER: PCT/US98/11422
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APPLICATION NUMBER: 60/048,876
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APPLICATION NUMBER: 60/048,880
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/049,020
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,916
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APPLICATION NUMBER: 60/048,949
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/049,375
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,892
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1). [384)
OTHER INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, corresponders INFORMATION: adding to amino acid residue 1 to 384 of Homo sapiens SPHK-1 of Ge OTHER INFORMATION: name sequence Accession Number AAF73423.
OTHER INFORMATION:
AUTHORS: Nava et al.
TITLE: Functional characterization of human spingosine kinase-1
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REFERENCE: 0732001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN NOS: 17
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Best Local Similarity 100.0%; Pred. No. 4.9e-235;
Matches 250; Conservative 0; Mismatches 0;
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Sequence 328, Application US/09205258

Sequence 128, Application US/09205258

GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 207 Human Secreted Proteins

FILE REFERENCE: PZ007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATABASE ACCESSION NUMBER: AAF73423
DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATABASE ACCESSION NUMBER: AFF73423
DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
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                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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PAGES: 81-84
DATE: 2000
                                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 384
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Matches 107; Conservative
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OTHER INFORMATION: Putative kinase sequence obtained by assembling sequences from s
OTHER INFORMATION: everal human ESTs (accession numbers D31133, AA232791, W63556, AA
OTHER INFORMATION: 081152 and AA026479).
NAME/KEY: MISC FEATURE
LOCATION: (1)..(204)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09796487
| Sequence 9, Application US/09796487
| Patent No. 683016|
| Patent No. 683016|
| GENERAL INPORMATION:
| APPLICANT: Spiegel, Sarah
| TITLE OF INVENITON: Sphingosin Kinase, Cloning, Expression and Methods of Use PILE REFERENCE: 073200101a (2033957-0001)
| CURRENT APPLICATION WUMBER: US/09/796,487
| CURRENT APPLICATION NUMBER: US 60.186,532
| PRIOR FILING DATE: 2000-03-03
| PRIOR FILING DATE: 2000-03-03
| PRIOR FILING DATE: 2000-05-05
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 9
| LENGTH: 204
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                                                                                                                                                                                                                                                                                                                                                . LOCATION: (36)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-205-258-328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 QVTNEDLLTNCTLLLCRRLLSPANLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAME 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 GEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
54.4%; Score 209; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.3e-195;
Matches 209; Conservative 0; Mismatches 0; Indels
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
SOFTWARE: PARCHIN NUMBER: 60/094,657
SOFTWARE: PARCHIN NOS: 1227
SOFTWARE: PARCHIN VET: 2.0
                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: SITE
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US-09-796-487-9
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1 INPRGGKGKALOLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALVVMSG
                                                    21 INPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALVVMSG
   Gaps
   ö
                                                                                                                                                                                                             61 DGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYE 107
                                                                                                                                                                           DGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYE 127
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER PELING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER PILING DATE: 1997-06-06
EARLIER PELING DATE: 1997-06-06
   0; Mismatches
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R APPLICATION NUMBER: 60/048,892
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,915
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,019
R R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,970
RR FILING DATE: 1997-06-06
RR APPLICATION NUMBER: 60/048,970
RR FILING DATE: 1997-06-06
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R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,899
R APPLICATION NUMBER: 60/048,899
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R APPLICATION NUMBER: 60/048,881
R FILING DATE: 1997-06-06
R PILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,896
R PILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,875
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,894
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,900
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APPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/048,895
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APPLICATION NUMBER: 60/048,884
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RESULT 12
US-09-796-487-5
US-09-796-487-5
Sequence 5, Application US/09796487
Sequence 5, Application US/09796487
Sequence 5, Application US/09796487
Sequence 5, Application US/09796487
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT PILING DATE: 2001-03-02
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: US 09/530,868
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100.0%; Pred. No. 2.1e-24;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 Length 63;
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8.6%; Score 33; DB 4; Le Best Local Similarity 100.0%; Pred. No. 2.1e-24; Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: PITSON, Stuart M
APPLICANT: Brian, WATTENBERG W
APPLICANT: Brian, WATTENBERG W
APPLICANT: Brian, WATTENBERG W
APPLICANT: Richard, D'ANDREA J
APPLICANT: Jennifer, BAMBLE R
APPLICANT: Jennifer, BAMBLE R
APPLICANT: Mathew, VADAS A
TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
FILE REPERENCE: PITSON-I
CURRENT APPLICATION NUMBER: PCT/AU00/00457
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: AU PQ 0339
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-08
NUMBER OF SEQ ID NOS: 56
NUMBER OF SEQ ID NOS: 56
SEQ ID NO 21
LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 109
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PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: AU PQ 0339
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: AU PQ 1504
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 63
TYPE: PRI
TYPE: PRI
CORGANISM: MUS MUSCULUS
US-09-959-897-13
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Patent No. 6730480
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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US-09-959-897-21
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids PEATURE:
NAME/FURE:
LOCATION: (97)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE
1 LOCATION: 1103)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-788
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14.3%; Score 55; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.4e-45;
Matches 55; Conservative 0; Mismatches 0; Indels
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APPLICANT: BISON, Stuart M
APPLICANT: Brian, WATTENBERG W
APPLICANT: Brian, WATTENBERG W
APPLICANT: Richard, D'ANDREA J
APPLICANT: Jennifer, BANBLE R
APPLICANT: Mathew, VADAS A
ITLE OF INVENTION: SPHINGOSINE KINASE ENZYME
FILE REPERENCE: PITSON-I
CURRENT APPLICATION NUMBER: US/09/959,897
CURRENT FILING DATE: 2001-11-13
                                                                          EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILLING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PELING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-16-06
EARLIER PILING DATE: 1999-07-15
EARLIER PILING DATE: 1999-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
SOFTWARE: PARENTON INVERE: 60/094,657
SOFTWARE: PARENTING VOICE: 1227
SOFTWARE: PARENTING VOICE: 2.0
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                               FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,917
                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
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; Patent No. 6730480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
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US-09-959-897-13
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ORGANISM: Mus musculus
PEATURE:
ORGANISM: MISC FEATURE
LOCATION: (1)...(381)
OTHER INPORMATION: SEQ ID NO 4 is the peptide sequence of mSPHKla in Figure 3, corre
OTHER INPORMATION: Sponding to amino acid residue 124 to 504 of SPHKla of GenBank se
OTHER INFORMATION: quence Accession Number AF068748. SEQ ID NO 4 is equivalent to SE
OTHER INFORMATION: Q ID NO 1 that is the amino acid sequence of SPHKla in Figure 1.
PUBLICATION INFORMATION:
AUTHORS: Kohama et al.,
TITLE: Molecular cloning and functional characterization of murine sphingosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09796487
Sequence 4, Application US/09796487
Patent No. 6830916
Batent No. 6830916
Batent No. 1000016
Batent No. 1000016
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use TILE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT PILING DATE: 2001-03-02
PRIOR PELLOR PERIOR OF 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SCOTTWARE: Patentin version 3.1
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100.0%; Pred. No. 1.1e-23;
tive 0; Mismatches 0; Indels
8.6%; Score 33; DB 4; Length 381;
100.0%; Pred. No. 1.1e-23;
                                                      Indels
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                                                                                                                                              76 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 108
                                                                                                              77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 109
                   100.0%; Prea. w..
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DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124) .. (504)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124) .. (504)
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Patent No. 6610534
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                                                           33; Conservative
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        Query Match
Best Local Similarity
Matches 33; Conserva
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PAGES: 23722-23728
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US-09-970-516-6
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US-09-796-487-4
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OTHER INFORMATION: BODDING to amino acid residue 124 to 504 of SPHKla of GenBank seq
OTHER INFORMATION: ponding to amino acid residue 124 to 504 of SPHKla of GenBank seq
OTHER INFORMATION: uence Accession Number AAC61697. SEQ ID NO 1 is equivalent to SEQ
OTHER INFORMATION: ID NO 4 that is the amino acid sequence of mSPHKla in Figure 3.
PUBLICATION INFORMATION:
AUTHORS: Kohama et al.
TITLE: Molecular cloning and fuctional characterization of murine sphingosin
                                                                                                                                                                                                       PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)._(373)

OTHER INFORMATION: SEQ ID NO 5 is the peptide sequence of Mouse SPHKIa in Fig. 2, co OTHER INFORMATION: SEGOND OTHER INFORMATION: rresponding to amino acid residue 131 to 504 of SPHKIa of GenBank OTHER INFORMATION: sequence Accession Number AAC61697.
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CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
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Best Local Similarity 100.0%; Pred. No. 1.1e-23;
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RELEVANT RESIDUES: (124)..(504)
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GENERAL INFORMATION:
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Bandras H., Micchika K., Ishibahii T., Yamashita H., Mutzakawa K.,

R. Wanasahi M., Micchika H., Kanihani H. T., Wamashita H., Mutzakawa K.,

R. Wanasahi M., Micchika H., Kalibahii T., Yamashita H., Mutzakawa K.,

R. Manno J., Kalibas K., Ishibahii T., Yamashita H., Tansa T. Toliba Y.,

R. Manno J., Kalibas S., Komai F., Hara R., Matchanba, H., Histora B., Chiba Y.,

R. Manno J., Kalibani H., Kanasha B., Manno M., Sakoba H.,

R. Mohikawa X., Sahoh A., Mizcopili H., Goo Y., Shihata B., Makaba B.,

M. Mohikawa Yamashinana H., Kalibahii P., Hara H., Takani S.,

M. Mohikawa Yamashinana H., Kalibahii P., Hara H., Takani S.,

M. Mohikawa X., Sahoh A., Mizcopili H., Goo Y., Shihata B., Makaba B.,

M. Mohikawa S., Sahoh A., Mizcopili H., Goo Y., Shihata B.,

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M. Mishapak H., Matanabe K., Mannada M., Takani S., Trakani B.,

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M. Mishamazaki M., Watanabe K., Wanano T., Wanano T., Wanashi M.,

M. Misha K., Yanga T., Namura Y., Manno T., Wanano T., Wanashi M.,

M. Manno J., Saho T., Shirai Y., Takhashi T., Sapano B.,

M. Mohamia Sugano J., Saho T., Shirai Y., Takhashi Y., Namashita R.,

M. Mohamia Sugano J., Saho T., Shirai Y., Takhashi Y., Namashita R.,

M. Mohamia Sugano J., Saho T., Shirai Y., Takhashi Y., Namashita R.,

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M. Mohamia Sugano J., Saho T., Shirai Y., Takhashi Y., Namashita R.,

M. Mohamia Sugano J., Saho J., Shirai J., Manno J., Saho T.,

M. Mohamia Sugano J., Saho J., Shirai M., Manno Y., Yamashita R.,

M. Mohamia Sugano J., Saho J., Shirai J., Manno J., Saho J., Jaho A., Shirai M., Manno J., Saho J., Jaho A., Shirai M., Manno J., Saho J., Jaho A., Shirai M.,

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X ENGUNE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A STRANDBERG RL., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McDwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodersten B., Kodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Pfam, PP00781; DAGK_cat; 1.
ProDom; PD005043; DAGKC; 1.
SMART; SM00046; DAGKC; 1.
ATP-binding; Calmodulin-binding; Kinase; Transferase.
CONFLICT 11 15 LRPRC -> ARL (in Ref. 4).
CONFLICT 114 115 NA -> KR (in Ref. 4).
CONFLICT 260 260 V -> I (in Ref. 4).
CONFLICT 260 260 V -> I (in Ref. 2).
CONFLICT 302 302 L -> P (in Ref. 2).
CONFLICT 31 37 37 V -> M (in Ref. 2).
CONFLICT 32 325 V -> G (in Ref. 4).
CONFLICT 32 325 V -> G (in Ref. 4).
CONFLICT 32 325 V -> G (in Ref. 4).
CONFLICT 337 337 V -> M (in Ref. 3).
SEQUENCE 384 AA; 42517 MM; EB04A7F2034C2DB0 CRC64;
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Last annotation update)
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Matches 336; Conservative
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01-OCT-2002 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
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Name=SPHK1;
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 SEKYRRIGEMRFTLGTFIRLALALRTYRGRLAYLPVGRVGSKTPASFVVVQQGPVDAHLVP
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R GO; GO:0005624; C:cytosol; ISS.

R GO; GO:0007050; F:D-erythro-sphingosine kinase activity; ISS.

R GO; GO:0007242; P:intracellular signaling cascade; ISS.

R GO; GO:0007242; P:intracellular signaling cascade; ISS.

R GO; GO:0007242; P:intracellular signaling cascade; ISS.

R InterPro; IPR001295; AldO/ket_red.

R InterPro; IPR001206; DAGKc.

R PFDOM; PD005043; DAGKc; 1.

R SMART; SM00046; DAGKc; 1.

R PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
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Submitted (SRP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC030553; AAH30553.1; -.
EMBL; BC014439; AAH14439.1; -.
                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 AA; 51084 MW; 5172E93A38C7CC17 CRC64;
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Last annotation update)
                                                                                                                                                 and mouse oDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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100.0%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 336; Conservative
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                             SPHK1 protein (Fragment).
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                                                                                                        Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Boateleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnnori P., Prange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnnori P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Brownstein M.J., Widnin T.B., Tooshiyuki S., Carnnori P., Prange C.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
A Jones S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009419; AAH09419.1;
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GO; GO:0005629; C:cytcosol; ISS.
GO; GO:000287; F:D-erythro-sphingosine kinase activity; ISS.
GO; GO:0000287; F:megnesium ion binding; ISS.
GO; GO:000742; P:intracellular signaling cascade; ISS.
GO; GO:00046521; P:sphingoid catabolism; ISS.
InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR001206; DAGKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.7%; Score 333; DB 2; Length 398; 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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ProDom; PD005043; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
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                                                              SEQUENCE FROM N.A.
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A Strausberg R. L., Feingold E. A., Grouse L. H., Derge J. G.,

A trausberg R. D., Colling F. S., Wagner L., Shenmen C.M., Schuler G.D.,

A tlaschul S. F., Zeeberg B. Buetow K. H., Schaefer C. F., Bhat N.K.,

A tlaschul S. F., Zeeberg B. Buetow K. H., Schaefer C. F., Bhat N.K.,

A physing R.F., Jordan H., More T. Max S. I., Wang J., Hsieh F.,

A papleron M., Soares M. B., Bonaldo M.F., Casavant T. E., Scheetz T. B.

Brownstein M.J., Usdin T. B., Tochhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunsarene P. H.,

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Raheby J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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Rakebley R. W., Touchman J. W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"We man and man 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 ASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ASGLRLFSVLSLAMGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 4.7e-230;
318 LAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKG 350
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100.0%; Pred. No. 4...
0; Mismatches
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PRT;
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ProDom; PD005043; DAGKC; 1.
SMART; SM00046; DAGKC; 1.
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Matches 125, Conservative
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Name=Sphk1;
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01-DEC-2001
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181
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                                                                                                                                                                                                                                                                             A REDAILEMES 2218825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Selminen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Boraldo M.F., Schaefer C.F., Bhat N.K., Barchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carminci P., Frange C., Rapleton M.J., Usdin T.B., Tochiyuki S., Carminci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abramson R.J., Hulyk S.W., Abramson R.J., McKernan R.J., Madan A.M., Gay L.J., Hulyk S.W., Arner S., Woltley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Abramson R.D., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Annienski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., Sochentz L., Schmutz J., Myers R.M., Butterfield Y.S., Abramson R.J., Marra M.A., Sochentz L., Schentz M.J., Schmutz J., Myers R.M., Schein J.E., Schnerch A., Schein M.J., Sanlaka U., Smailus D.E., Schnerch A., Schein J.E., Annie R.M., A
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008040; AA408040.1; -.
GO; GO:0005629; C::Membrane fraction; ISS.
GO; GO:000529; C::Membrane fraction; ISS.
GO; GO:0007242; F::Megresium ion binding; ISS.
GO; GO:0007242; P::Magresium ion binding; ISS.
GO; GO:00046521; P::Magnesium ion binding; ISS.
GO; GO:0046521; P::Magnesium ion binding; ISS.
RO; GO:0046521; P::Magnesium ion binding; ISS.
RO; GO:0046521; Aldovket_red.
InterPro; IPR001206; DAGKC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSTIE; PRO0065; DAGKC; 1.
PROSTIE; PRO0063; ALDOKETO REDUCTASE 3; UNKNOWN 1.
                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                       384 AA
                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00781, DAGK cat; 1.
ProDom; PD005043; DAGKc; 1.
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Best Local Similarity 99.77
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
                                                       PRELIMINARY;
                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                               SPHK1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 CRVLVLINPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDA
                          15 CRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDA
SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
                                                                                                   LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Unnamed protein product.
Unnamed protein product.

Bacaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005829; C:cyto801; ISS.
GO; GO:0005624; C:membrane fraction; ISS.
GO; GO:000056; F:D-erythro-sphingosine kinase activity; ISS.
GO; GO:000287; F:magnesium ion binding; ISS.
GO; GO:0007242; P:intracellular signaling cascade; ISS.
GO; GO:004621; P:phingoid catabolism; ISS.
InterPro; IPR001295; Aldo/Ket_red.
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100.0%; Pred. No. 5.9e-116;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00063; ALDOKETO REDUCTASE 3; UNKNOWN 1.
SEQUENCE 329 AA, 36393 WW; 7F430ABDOCASFDC7 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                  301 RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKG 336
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(TrEMBLrel. 19, Last seq
(TrEMBLrel. 26, Last ann
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01-OCT-2000 (TrEMBLrel. 15, Last seq
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EMBL; BC037710; AAH37710.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                  Kinase.
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XX STRAINE-EVBN/N; TISSUE-Kidney;

XX STRAINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Staubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Stauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

XX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Bosak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

XX Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Norley W., Touchman J.W., Gaergren E.J., Lu X., Gibbs R.A.,

XX Haldon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Haldon A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX RIZYAHISKI M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Hones S.J., Marra M.A.,

XX Hones S.J., Marra M.A.,

XX Hones S.J., Marra M.A.,

XX HONES C.D., Marra M
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                         GO; GO: 0005829; C: Cytosol; ISS.
GO; GO: 0005829; C: Cytosol; ISS.
GO; GO: 0005624; C: membrane fraction; ISS.
GO; GO: 0017050; F: D-erythro-sphingosine kinase activity; ISS.
GO; GO: 0000287; F: meagnesium ion binding; ISS.
GO; GO: 0007242; P: intracellular signaling cascade; ISS.
GO; GO: 0007242; P: intracellular signaling cascade; ISS.
Framp. PF00781; DRGK cat; D.
ProDom; PD005043; DAGKC; 1.
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                                                                                                                                      SEQUENCE FROM N.A.
Thompson D., Pyne S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF415213 AALO/1499.1; -.
MGD; MGI:1316649; SphkI.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 AA; 42344 MW; 2F2C1F10D59EB129 CRC64;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Le
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STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00046; DAGKC; 1.
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  musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=10090;
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01-MAR-2004
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Q8CI15;
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CQGCI15
CQGCI15
CQGCI15
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MGD; MGI:1116649; SphKI.

GO; GO:0005829; C:cytcsol; ISS.
GO; GO:0005824; C:cytcsol; ISS.
GO; GO:0007524; C:membrane fraction; ISS.
GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
GO; GO:0007287; F:magnesium ion binding; ISS.
GO; GO:0007242; P:intracellular signaling cascade; ISS.
GO; GO:000521; P:sphingoid catabolism; ISS.
FinterPro; IPR001206; DAGKc.
PFam; PF00781; DAGK cat; 1.
ProDom; PD005043; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 33; DB 2; Length 382;
100.0%; Pred. No. 7.4e-24;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 8.6%; Score 33; DB 2; Length 388; Local Similarity 100.0%; Pred. No. 7.5e-24; Pres 33; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        382 AA; 42443 MW; B791FAA58FCE3D29 CRC64;
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GO: 000104143; P: Giazoylglycerol kinase activity; IEA.
GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 AA; 43254 MW; 01EB032322542CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 AA.
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EMBL; AF068749; AAC61698.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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01-NOV-1998 (TYEMBLrel. 08, Cre
01-NOV-1998 (TYEMBLrel. 08, Las
01-MAR-2004 (TYEMBLrel. 26, Las
Sphingosine kinase (Fragment)
Name=Sphkl; Synonyms=SPHKla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Sphk1; Synonyms=SPHK1b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 08, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00781; DAGK cat; 1.
ProDom; PD005043; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                                                                                                                       SMART; SM00046; DAGKc; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD005043; DAGAC;
SMART; SM00046; DAGKC; 1
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98 98

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77 VMSGDGLMHEVVNGLMERPDWE
                   77 VMSGDGLMHEVVNGLMERPDWE
                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                             Sphingosine kinase 1.
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                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                               25-OCT-2004
                                                                                                                                                                                                                                                                                               Name=Sphk1;
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Q8Y1S2;
                                                                                                                                                                                         Q642F6;
                                                                                                                                                                     Q642F6
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08Y1S2
1D QBY1S;
AC QBY1S;
DT 01-MAD
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                                                                                                       SEQUENCE FROM N.A. MEDLINE=9835082; PubMed=9726979; DOI=10.1074/jbc.273.37.23722; MEDLINE=9835082; PubMed=9726979; DOI=10.1074/jbc.273.37.23722; Kohama T., Olivera A., Edsall L., Nagiec M.M., Dickson R., Spiegel S.; Molecular cloning and functional characterization of murine sphingosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A SINGOR N.;

methylation status and multiple alternative first exons.";

Genomics 78:117-125(201).

EMBC, AB049575; BAB62324.1; -.

EMBL; AB049573; BAB62320.1; -.

EMBL; AB049573; BAB62321.1; -.

REMBL; AB049573; BAB6232.1; -.

REMBL; AB049573; BAB6232.1; -.

REMBL; AB049574; BAB6232.1; -.

REMBL; AB049574; BAB6232.1; -.

REMBL; AB049577; BAB6232.1; -.

ROG; GO:00005829; C:cytcsol; ISS.

ROG; GO:0007050; F:megnesium ion binding; ISS.

RO; GO:0007050; F:megnesium ion binding; ISS.

RO; GO:0007051; P:sphingoid catabolism; ISS.

ROG; GO:0046521; P:sphingoid catabolism; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Imamura T., Ohgane J., Ito S., Ogawa T., Hattori N., Tanaka S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 2; Length 383;
Pred. No. 7.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.6%; Score 33; DB 2; Length 504;
100.0%; Pred. No. 9.3e-24;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                      J. Biol. Chem. 273:27722-23728 (1998).

EMBL, AF068748, AAC61697.1; -.

MGD, MGI:1316649, Sphkl.

GO; GO:000413; F:diacylglycerol kinase activity; IEA.

GO; GO:007205; P:protein kinase C activation; IEA.

InterPro; IPR001206; DAGKc.

ProDom; PD005043; DAGK cat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 AA; 55119 MW; 2AAFEBA72027F509 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Sphingosine kinase 1f (Sphingosine kinase 1a) (Sphingosine kinase 1a) (Sphingosine kinase 1a).
Name=sphklf; Synonyms=sphkla, sphklc, sphkle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 VMSGDGLMHEVVNGLMERPDWETAIOKPLCSLP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD005043; DAGKc; 1.
SMART; SM00046; DAGKc; 1.
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00046; DAGKC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shiota K.;
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SEQUENCE
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TISSUE-Testis,

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                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PROBABLE SIGNAL PEPTIDE PROTEIN.
Name-RS01518; OrderedLocusNames-RSC0617;
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 22; DB 2; Length 383;
100.0%; Pred. No. 7.5e-13;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Director MGC Project;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC081738; AAH81738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 AA; 42432 MW; 70B6E217AF812F77 CRC64;
                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
383 AA.
                                                                                                     Created)
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PRT;
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                                                                                                                                                     (TrEMBLrel. 28, (TrEMBLrel. 28,
                                                                                                     28,
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es 22; Conservative
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TISSUE=Carcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suziki Y., Nagai K., Sugano S., Ishiis S., Kawai.Hio Y., Salto K., Suziki Y., Nagai K., Sugano S., Ishiis S., Kawai.Hio Y., Salto K., Wamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                            Salanoubat M., Genin S., Arriguenave F., Gouzy J., Mangenot S., Arliguenave F., Gouzy J., Mangenot S., Charlet M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Cloudel-Renard C., Cunnac S., Demange N., Saguier P., Lave M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                           2.3%; Score 9; DB 2; Length 118;
100.0%; Pred. No. 2.9;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9; DB 2; Length 244;
Pred. No. 5.3;
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                                                                                        MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .601; BAC11085.1; -.
244 AA; 24989 MW; F11285DC202EFC43 CRC64;
                                                                                                                                                                                                                                                                                                                                                118 AA; 12054 MW; 955D9DEA2C16CF42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ90120
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NRAO; Q9BRN1; Q9H0Q2; Q9NWU7; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 05-JU-2004 (Rel. 44, Last annotation update) Sphingosine kinase 2 (EC 2.7.1.-) (SK 2) (SPK 2).
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100.0%; Pred. No. s.c..
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
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es 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 AGSGNALAA 118
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                                                                                                                                                                                                                                                                                                                          Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                             SEQUENCE FROM N.A.
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NCBI_TaxID=305;
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0802M3
AC 0802M
AC 0802M
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DT 01-0C
DE HYPOT
OS EURAT
OC MAMMO
OC EURAT
OC MAMMO
OC RAMMO
CO NON (1)
RP SEQUE
RA SUZUK
RA SUZUK
RA SUZUK
RA HATTO
SR HATTO
SR HATTO
SR SUDMI
SR MASHUM
RA HATTO
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RESIDENCE FROM NA. (1900/00042), AND COLLOLO14/jbc.MOD295200;
RAILEL SOUTHER TRANS NA. (1900/00042), AND COLLOLO14/jbc.MOD295200;
RAILEL SOUTHER NA. NAWAY VE. Reball LC., Kodon K., Poulton S., Miletler S., Kobasa T., Spiegel S., Targeteriazion of a novel RT William S., Collone N., Spiegel S., Miletler S., Kobasa T., Spiegel S., Targeteriazion of a novel RT William S., Spiegel S., Miletler S., Kobasa T., Spiegel S., Miletler S., Kobasa T., Spiegel S., Miletler S., Kobasa T., Spiegel S., Miletler M., Spiegel S., Miletler M., Spiegel S., Spiegel S., Spiegel S., Spiegel S., Miletler M., Spiegel S., Spie
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EMBL; AF245447; AAF74124.1; -.
EMBL; AL136701; CAB66636.1; -.
EMBL; BC006161; AAH06161.1; -.
EMBL; BC010671; AAH10671.1; -.
EMBL; AK000599; BAA91280.1; -.
Genew; HGKC.18859; SPHKZ.
H-INVDB; HXX0012297; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00781; DAGK cat; 1.
ProDom; PD005043; DAGKc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00046; DAGKc;
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654 AA;
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                                                                           CDNAB."
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SOLUTION SERVICE SERVI
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Search completed: June 15, 2005, 12:22:24
Job time : 209 secs
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/FITd=VSP 006217.

/FITd=VSP 006217.

/FITd=VSP 006217.

/FITG=VSP 006217.

GRLSYLAPATHORSALLCRGGGHPLDLLSVTLASGSRCFSF LSVAMGFVSTVD1GSBFRALGSARFTLGTVGLATHTYR GRLSYLPAATHORSCPLLPQQLALGFSRFIGDRVNGGGRIG SILCRGHTQRTLPAAREGGGSLFLKNINVFICKKKKK (in isoform 3).

/FITG=VSP 006218.

/FITG=VSP 006218.

/FITG=VSP 006218.

/FITG=VSP 006218.

/FITG=VSP 006218.

/FITG=VSP 006218.
Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                Nat. Genet. 36:40-45(2004).

-!- PUNCTION: Catallyzes the phosphorylation of sphingosine to form ephingosine 1-phosphate (SPP), a lipid mediator with both intra-
sphingosine 1-phosphate (SPP), a lipid mediator with both intra-
and extracellular functions. Also acts on D-erythro-
dihydrosphingosine, D-erythro-sphingosine and L-threo-
dihydrosphingosine.
-!- CATALYIIC ACTIVITY: Sphingosine + ATP = sphingosine 1-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bvent=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005829; C:cytosol; IEP.
GO; GO:0005829; C:cytosol; IEP.
GO; GO:0005624; C:membrane fraction; IEP.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0017016; F:Ras interactor activity; NAS.
GO; GO:0008481; F:sphinganine kinase activity; NAS.
GO; GO:0006816; P:sphinganine kinase activity; NAS.
GO; GO:0006816; P:sphinganine-1-phosphate biosynthesis; NAS.
InterPro; IPR0071206; DAGKc.
InterPro; IPR007110; Ig-like.
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-!- SIMILARITY: Contains 1 DAGKc domain.
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Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekwaka, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Perpstra, P.; Togoni, A.; Tosato, V.; Uchiyama, T.; Minters, P.; Wipet, A.; Yamamoto, H.; Yamamote, K.; Yasumoto, K.; Yoshida, K. A; Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A. A.; Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:034799; GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14972.1
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33616
R;Pinol-Roma, S; Swanson, M.S.; Gall, J.G.; Dreyfuss, G.
C, Cell Biol. 109, 2575-25897, 1899
A;Title: A novel heterogeneous nuclear RNP protein with a unique distribution on nascent A;Reference number: A33616; MUID:90078296; PMID:2687284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P14866; GB:X16135; NID:g32355; PIDN:CAA34261.1; PID:g32356 C;Superfamily: Caenorhabditis elegans hypothetical protein C44B7.2
                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-309 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:C49H3.5
A;Introns: 12/3; 35/3; 67/3; 174/3; 208/3; 266/2; 288/1; 310/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-812 <WUX>
A;Cross-references: EMBL:U42436; PIDN:AAA83485.1; CESP:C49H3.5
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                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Wu, X.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C49H3.
A;Reference number: Z21485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - Caenorhabditis elegans
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A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 8; DB 2;
100.0%; Pred. No. 16;
ive 0; Mismatches
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100.0%; Pred. No. 23;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 8; DB 2
100.0%; Pred. No. 9.4
ive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-558 <PIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A33616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
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CiSpecies: Pseudomonas aeruginosa
CiSpecies: Pseudomonas aeruginosa
CiSpecies: Dseudomonas aeruginosa
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CiSpecies: Dseudomonas aeruginosa
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Attrie: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A; Accession: H83627
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: LOSP & STO>
A; Residues: 1-208 & STO>
A; Experimental source: strain PA01
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High protein ytlR - Bacillus subtilis

Lispeciaes Bacillus subtilis

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Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

Rikunst, F.; Ogasswara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, Nature 390, 249-256, 1997

Richtors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurifet, R.; Lapidus, A.; Laudinois, A.; Laudhors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Lervine, A.; Liu, H.; Masuda, S.; Maueell

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
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hypothetical prote
putitive HlyD fami
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CT700 hypothetical
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probable glutamine
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A, Genetics:
A, Genetics:
C, Superfamily: Schizosaccharomyces pombe hypothetical protein SPCC191.05c
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100.0%; Pred. No. 6.6;
tive 0; Mismatches
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F86595
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Best Local Similarity
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CjAccession: AF3030
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells; Karp, P.; Romero, P.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Atthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
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A.Molecule type: DNA
A.Molecule type: DNA
A.Rosidues: 1-89 *WIL>
A.Status: DBJ *WIL>
A.Status: DBJ *WIL>
A.Status: DBJ *WIL>
A.Status: CABO7692.1; GSPDB:GN00020; CESP:Y46
A.Status: CABO7692.1; GSPDB:GN00020; CESP:Y46
A.Experimental source: clone Y48E1B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:08U978; GB:AE008689; PIDN:AAL44660.1; PID:917742285; GSPDB:GPA;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Atu3850 [imported] - Agrobacterium tumefaciens (strain CS8, Dupont) C.Species: Agrobacterium tumefaciens C.Species: Agrobacterium tumefaciens C.Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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Ayîtile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF3030
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27015
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1.8%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 23; ive 0; Mismatches
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A,Reference number: 220299
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Best Local Similarity 100. Matches 7; Conservative
    Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                 23 PRGGKGK 29
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A Molecule type: DNA
A, Residues: 1-87 < KUR>
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A;Gene: CESP:Y48E1B.6
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                                                                                                                                                                                                                                                                                                                       protein kinase (EC 2.7.1.37), cGMP-dependent 2, type 1 [similarity] - fruit fly (Drosoph N;Contains: protein kinase, cGMP-dependent 2, type 3; protein kinase, cGMP-dependent 2, c;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 05-May-2000 #sequence revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B34106; B34106; F34106
R;Kalderon, D.; Rubin, G.M.
J. Biol. Chem. 264, 10738-10748, 1989
A;Title: CGMP-dependent protein kinase genes in Drosophila.
A;Reference number: A34106; MUD:89278147; PMID:2732245
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C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
R;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
R;Date: C:: Method C:: 
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A;Residues: 1-62 <BUL>
A;Cross-references: UNIPROT:P54028; GB:U67480; GB:L77117; NID:g2826265; PIDN:AAB98237.1;
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A;Residues: 1-1088 <KML>
A;Cross-references: UNIPROT:Q03043; GB:M27117; GB:M27118; GB:M27119; GB:M27120; NID:g157
A;Note: the authors translated the codon AGG for residue 692 as Thr
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A;Residues: 521-691,'T',693-1088 <KA3>
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Molecule type: DNA; mRNA
Residues: 347-507,'S',508-691,'T',693-1088 <KA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: FlyBase:for
A,Cross-references: FlyBase:FBgn0000721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 HTASGLRL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 HTASGLRL 242
                                                                                                                                                   217 AEAEISFT 224
                                                                  43 AEAEISFT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: E34106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: F34106
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hypothetical protein - Deinococcus radiodurans (etrain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Accession: G73308
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maß, S.; Sahit, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast 10, 1657-1662, 1994

A;Title: Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of ye A;Reference number: S50701; MUID:95242842; PMID:7725802

A;Accession: S50770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT: P40895; EMBL: Z34098; NID: 9496934; PIDN: CAA83996.1; PID: 949699; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994 R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. submitted to the Protein Sequence Database, September 1995 A;Reference number: S56835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z49490; NID:g1015601; PIDN:CAA89512.1; PID:g1015602; MIPS:YJL21E
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9RSG8; GB:AE002049; GB:AE000513; NID:g6459945; PIDN:AAF1171(
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A,Reference number: A75250; MUID:20036896; PMID:10567266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ц,
                                                                                                                                                                                                                                                                                                                             hypothetical protein VJL215c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein HRE119; hypothetical protein J0231
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1991 #sequence revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S50770; S57005; S45158
R;Vandenbol, M; Durand, P; Bolle, P.A; Dion, C; Portetelle, D; Hilger,
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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C;Superfamily: Deinococcus radiodurans hypothetical protein DR2156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-119 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 119;
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              Indels
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C;Superfamily: Saccharomyces hypothetical protein YJL215c
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5. 44;
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100.0%; Pred. No. 41;
tive 0; Mismatches
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1.8%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches
              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 7; Conservative
              7; Conservative
                                                                                  177 VDLESEK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 LLNPRGG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 ADVDLES 181
                                                                                                                                                 32 VDĽESEK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 LLNPRGG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-119 <VAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-128 <WHI>
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A;Molecule type: DNA
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              Matches
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C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: 199254
R;Goodner, B:, Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A: Liu, F:; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q8U978; GB:AE007870; PIDN:AAK89562.1; PID:g15159447; GSPDB:d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tegical Chain C3 region - mouse (fragment)
C1Species: Mus musculus (house mouse)
C1SPECIES: Musculus (house mouse)
C1SPECIES: Musculus (house mouse)
C2SPECIES: Musculus (house)
C2SPECIES: Musculus (ho
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: 168730
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid A;Reference number: 154443; MUID:88152907; PMID:3346043
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;Cross-references: GB:M22933; NID:g194464; PIDN:AAA37915.1; PID:g194469; Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 7; DB 2;
100.0%; Pred. No. 34;
tive 0; Mismatches
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100.0%; Pred. No. 37;
trive 0; Mismatches
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A;Map position: linear chromosome
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <KUR>
                                                                                                                                                                                                                                                                                               A; Accession: H98254
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R1.

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A;MOIGCUIE LYPE: MRNA
A;Residues: 1-139 <ROB.
A;Cross-references: UNIPROT:P33575; GB:L05925; NID:g213209; PIDN:AAA49269.1; PID:g213210
A;Note: sequence extracted from NCBI backbone (NCBIP:122170)
A;Accession: A45051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-85,105-139 <R02>
A; Residues: 1-85,105-139 <R02>
A; Cross-references: GB:L05924; NID:g213207; PIDN:AAA49268.1; PID:g213208
A; Note: sequence extracted from NCBI backbone (NCBIP:122166)
C; Comment: These forms are encoded by a different gene than B45051; we have arbitrarily
C; Superfamily: lamprin
C; Superfamily: lamprin
C; Keywords: alternative splicing; cartilage; extracellular matrix
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-139/Product: lamprin 2, long splice form #status predicted <WATI>
F; 20-85,105-139/Product: lamprin 2, short splice form #status predicted <MATI>
                                                                                       RESULT 14
825119
histone H2A - Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S25119; S33211
R;Lopez M.C.
submitted to the EMBL Data Library, July 1992
A;Reference number: S25119
A;Accession: S25119
A;Accession: S25119
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A;Residues: 1-135 *LOb>
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A;Cross-references: EMBL:X67287; NID:g10617; PIDN:CAA47703.1; PID:g10618
C;Superfamily: histone H2A
C;Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus
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c expression, functional activity or cellular functional activity of sphingosine kinase in a subject and also for treating a mammal by modulating the activity of SK. Diseases treated by regulating SK cellular activity include rheumatoid arthritis, asthma, atherosclerosis, cinflammation, meningitis, multiple sclerosis and septic shock  Sequence 384 AA;  Query Match  Sequence 384 AA;  Query Match  DispageRGVLPRPCRVIVLINPRGGKGRALQLFRSHVQPLIABABISFTLMLTERRNHA 60   Hill	241		34 361 MVSGCVEPPPSWKPQQMPPPEEPL 384	RESULT 2 ADF28783 ID ADF28783 standard; protein; 384 AA. XX	.C ADF28783; X 12-FEB-2004 (first entry)	X B. Human sphingosine kinase (hSK)1 protein sequence.	W SK; sphingopine kinase; phosphorylation; protein kinase; ERK1; ERK2; W CDK2; cytostatic; antiinflammatory; immunosuppressive; antiarthritic; antirheumatic; antiarteriosclerotic; antiasthmatic; human; hSK1; enzyme.	A. Homo sapiens.	T Key Location/Qualifiers T Modified-site 148 T /note= "phosphorylated"	Modified-site 181 /note= Modified-site 184	T. Modified-site 225 T Modified-site 250 T Modified-site 250 T Modified-site 250 T Modified-site 250	XX WO2003082322-A1.	D 09-0CT-2003.
2555558 2 2 3 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4	P 6	P 45	& 43 43	AD A XX	SXE	XE;	<b></b>	X S X	EEE	FEE	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	X & 3	₹ G X
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5 AAO20562 4 AAU41508 4 AAU41508 5 AAU71508 6 ABA22873 7 ADB60055 4 AA0812294 4 AA0812294 4 AA0812294 4 AA0812294 6 ABB99343 7 ABO74860 6 ABB99343 7 ABO74860 6 ABB65276 6 ABW65276 6 ABW65276 6 ABW65276 6 ABW65276 6 ABW65276 7 ADI60368 4 AAG70919 8 AAU75333 5 AAU75333 5 AAU75333 5 AAU75333 5 AAU75333 5 AAU75333 6 ABC70919 7 ABC70919 8 AAG70919 8 AAG70919	ALIGNMENTS	n; 384 AA.	st entry) kinase protein sequence	s; antiarthritic; antias neuroprotective; antiba			457.	SUS PTY LTD	, Xia P, D'		and nuc nent of ningiti	English.	phingosine kinas acids and modul
20		protein;	entry) .nase p	antia uropi			0WO-AU000457	NOSMHOL.	erg BW		nase cis an lamma	100pp; E	human sp nucleic
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		standard;	AAB4800 <i>7;</i> 19-MAR-2001 (first Human sphingosine ki	Sphingosine kinase; antiinflammatory; ne human.	Homo sapiens. WO200070028-A1.	-NOV-2000.	-MAY-2000; 2000WO	y S	, common a n SM, Watten MA;	2001-0162 B; AAC841	Novel sphingosine kinase protein diagnosis, prophylaxis and treate atherosclerosis, inflammation, meshock.	Claim 9; Fig 7a; 100	

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The invention relates to modulating sphingosine kinase (SK) functional activity. The method involves contacting the SK with an agent for a time and under conditions to modulate phosphorylation of the SK where inducing or agenizing the phosphorylation down regulates SK activity and inhibiting or antegonizing the phosphorylation down regulates SK activity. The modulation of the phosphorylation is modulation of prolinedirected protein kinase catalyzed phosphorylation. The proline-directed regulation. The methods and agents are useful for treating and/or regulation. The methods and agents are useful for treating and/or prophylaxis of a condition characterized by aberrant, unwanted or inappropriate cellular activity or sphingosine kinase functional cativity, e.g. a neophastic condition or an inflammatory condition such as rheumatoid arthritis, atherosclerosis, asthma, autoimmune disease or inflammatory bowel disease. The present sequence represents a human SK
                                                                                                                                                                                                                                                                             Modulating sphingosine kinase functional activity for treating arthritis, atherosclerosis and asthma by contacting the sphingosine kinase with an agent for a time and under conditions to modulate phosphorylation of the
                                                                                                                                                                                                    Wattenberg BW;
                                                                                                                                                                                                    Vadas MA,
                                                                                                                                                                                                    Verwey JR,
                                                                                                                                                                                                                                                                                                                                                                                     NO 12; 95pp; English.
                                                                                                                                                                                                    Moretti PA,
                                                      05-APR-2002; 2002AU-00001538.
08-APR-2002; 2002AU-00001621.
19-SEP-2002; 2002AU-00951668.
21-JAN-2003; 2003AU-00900230.
28-MAR-2003; 2003WO-AU000388.
                                        2002AU-00001448
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                                        28-MAR-2002;
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# Sequence 384 AA;

9 1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA Gaps ö Length 384; Indels .. 0 DB 7; 100.0%; Score 384; D 100.0%; Pred. No. 0; iive 0; Mismatches Conservative Local Similarity tes 384; Conser Query Match Best Loca Matches 유 ઠ

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AAB18659 standard; protein; 384 AA **4AB18659** 

AAB18659;

(first entry) 22-JAN-2001 human regulator of intracellular phosphorylation.

Human; intracellular phosphorylation regulator; HRIP; stroke; myelon neurological disorder; Parkinson's disease; demyelinating disease; meningitis; developmental disorder; neuromuscular disorder; cancer; mayasthenia gravis; cell proliferative disorder; actinic keratosis arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis; autoimmune disorder; inflammatory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus; rheumatoid arthritis; microbial infection; trauma.

Homo sapiens

 153
 note= "diacylglycerol kinase catalytic site" note= "potential phosphorylation site" 'note= "potential phosphorylation site" 'note= "potential phosphorylation site" 'note= "potential phosphorylation site" /note= "potential phosphorylation site" note= "potential glycosylation site" Location/Qualifiers 181 Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Active-site

WO200055332-A2

21-SEP-2000

17-MAR-2000; 2000WO-US007277.

99US-0135049P. 99US-0125593P. 18-MAR-1999; 09-JUL-1999; 10-MAY-1999;

(INCY-) INCYTE PHARM

Baughn MR, Azimzai Y; Hillman JL, Ή, Yue Tang YT, Au-Young J; Bandman O, Lu DAM,

WPI; 2000-602121/57.

N-PSDB; AAA75676.

neurological, Novel human intracellular phosphorylation regulator polypeptides and polymucleotides for diagnosis, prevention and treatment of neurologic cell proliferative and autoimmune/inflammatory disorders.

Claim 1; Page 77-78; 96pp; English.

The present sequence represents a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and antagonists of HRIP polypeptide. HRIP and its agonist or antagonist are useful for treating a disease or condition associated with decreased or increased expression of functional HRIP. Diseases treated or diagnosed include neurological disorders such as stroke, Parkinson's disease, demyelinating diseases, bacterial and viral meningitis and other disorders of the central nervous system, neuromuscular disorders, myasthenia gravis, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer including leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder, bone, bone marrow, liver, lung, muscle, ovary, autoimmune/ inflammatory disorder such as Addison's disease, acquired immunodeficiency diseases,

RESULT 3

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120
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                                                                                                                                                                                                                                                     SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
 allergies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial
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                                                             Length 384;
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, Otsuki T;
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, Sugiyama T, Wakamatsu A, Nagai K,
                                                    87.5%; Scott No. 0, 100.0%; Pred. No. 0, 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB94589 standard, protein, 384 AA
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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            infection and trauma
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                                                                       Similarity
                                     Sequence 384 AA;
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The present invention describes primer sets for synthesising 5602 full-

[ad an oligo-dr primer and an oligonucleotide complementary to the

complementary strand of a polynucleotide comprises one of the 5602

nucleotide sequences defined in the specification, where the

complementary strand of a polynucleotide which comprises one of the 5602

oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which complementary to the

complementary strand of a polynucleotide which complementary to a

polynucleotide comprises a 1'-and sequence, where the

complementary strand of sequence is selected from those defined in the

polynucleotide comprises at least 15 nucleotides and the combination of

the 5'-end sequence 31'-end sequence is selected from those defined in the

specification. The primer sets can be used in antisense therapy and in

complementary full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers are also useful for the

condas assily without any specialised methods. AAH03166 to AAH13628 and

AAH118613 to Path18742 repersent human cDNA sequences; AAB9244 to AAB95893

crepresent human amino acid sequences; and AAH13622 represent

oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASI 120
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 336; Conservative
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301 RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKG 336

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LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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, Otsuki T;
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Wakamatsu A, Nagai K,
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100.0%; Pred. No. v,
... 0; Mismatches
                                                                                            Nishikawa T,
                          27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
                  99JP-00248036
                                                      09-JUN-2000; 2000JP-00241899
28-JUL-2000; 2000EP-00116126
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Best Local Similarity
                                                                                                       Sugiyama
                                                                                            Isoqai T,
                                                                                                                                                                                                                                                                                                                                                                                                                   present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 384 AA;
                 29-JUL-1999;
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                                                                                                      Ishii S,
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Human; sphingosine kinase type 1; sk1; chromosome 17q25.2; sphingosine-1-phosphate; S1P; drug screening; therapy; haemostasis; thrombosis; allergic reaction; proliferative disease; cancer; haematopoietic disorder; leukaemia; cardiovascular disease; atroke; atherosclerosis; coronary artery disease; dyslipidaemia; diabetes; autoimmune disease; inflammatory disease; multiple sclerosis; r helper-1 related disease; chronic obstructive pulmonary disease; asthma; myocardial infarction; neurodegenerative disease; embryogenesis; anticoagulant; cerebroprotective; neuroprotective; antipsoriatic; antiarthritic; cytostatic; cardiant; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is human sphingosine kinase type 1 (hek1). The hek1 gene is located on chromosome 17q25.2. The sk1 converts the substrate sphingosine to sphingosine-1-phosphate (SIP). The sk1 gene and encoded polypeptide are applicable in screening drug candidates particularly inhibitors for preventing or treating disorders such as haemostasis, thrombosis, allergic reactions, proliferative diseases including cancer, haematopoietic disorders such as leukaenia, cardiovascular diseases such as stroke, atherosclerosis and coronary artery disease, dyslipidaemia, diabetes including type I and type II diabetes, autoimmune and inflammatory diseases such as multiple sclerosis, T helper-1 related diseases, chronic obstructive pulmonary disease, asthma, myocardial infarction, neurodegenerative disorders, natural wound healing processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human sphingosine kinase type I gene for screening drug candidates particularly inhibitors used for preventing or treating e.g. atherosclerosis, thrombosis, asthma and diabetes.
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100.0%; Pred. No. 0;
iive 0; Mismatches
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/label= Conserved_region
                                                                                                     Human sphingosine kinase type 1 (hskl).
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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AAE00924 standard; protein; 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0162307P
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                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and embryogenesis
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                                                                     04-JUL-2001
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1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60

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congestive heart failure; myocardial ischaemia; wound healing; ischaemia-reperfusion injury; peripheral arterial disease; angiogenesis; coronary artery disease; peripheral vascular disease; fracture repair; reconstructive surgery; transplantation; islet transplant; tendon repair; sports injury; ulcer; thromboangitis obliterans; Buerger's disease; periodontal tissue regeneration; radiotherapy-induced oesophagitis.
                                                                      180
                                                                                                                                                                                     SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                                                                                           241 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
                                                   RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
                                                                                                                     NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                    181 SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                                                                     LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new method of inducing blood vessel formation in an animal. The method of the invention involves administering sphingosine kinase to the animal. The method is useful for inducing blood vessel formation in an animal, or preventing or treating congestive heart failure, myocardial ischaemia, ischaemia-reperfusion injury and paripheral arterial diseases in an animal, e.g. mammal (such as primate including human). The invention is also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inducing blood vessel formation, or preventing/treating congestive heart failure, ischemia-reperfusion injury, myocardial ischemia and peripheral arterial diseases in animal, by administering sphingosine kinase.
sphingosine kinase 1; SPHK1; blood vessel formation; primate;
                                                                                                                                                                                                                                                                                                                                        RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKG 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG31586 standard; protein; 384
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N-PSDB; ABK90198.
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diseases or disorders selected from coronary artery disease, peripheral vascular disease, wound healing and fracture repair, reconstructive surgery, transplantation such as islet transplants, tendon repair/sports injury, healing of ulcers, thromboangitis obliterans (Buerger's disease), periodontal tissue regeneration and radiotherapy-induced oesophagitis. The present amino acid sequence represents the human sphingosine kinase I (SPHKI) protein as described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALOLFRSHVOPLLAEAEISFTLMLTERRNHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTIMLTERRNHA
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100.0%; Pred. No. 0;
iive 0; Mismatches
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2002US-0371075P.
2002US-0371507P.
2002US-0372984P.
2002US-0374194P.
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2002US-0385023P.
2002US-0388853P.
2002US-0389395P.
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                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                           Sequence 384 AA;
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10-APR-2002;
16-APR-2002;
19-APR-2002;
24-MAY-2002;
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14-JUN-2002;
17-JUN-2002;
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Matches 336;
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Marker gene related amino acid sequence SEQ ID NO:693.

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Disclosure; SEQ ID NO 26; 454pp; English.
                                                                                                Hunter JJ, Macbeth KJ, Tsai F, Williamson MW, Rudolph-Owen LA;
                                                                                                                                                                                                                                                                              protein 49863 of the invention.
                      22-AUG-2002; 2002US-0405155P.
27-AUG-2002; 2002US-0405161P.
25-CCT-2002; 2002US-0421195P.
12-NOV-2002; 2002US-0425456P.
19-NOV-2002; 2002US-0425456P.
10-DEC-2002; 2002US-0437122P.
       2002US-0397726P.
2002US-0403046P.
                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                          WPI; 2003-646176/61.
N-PSDB; ADE38364.
                                                                                                                                                                                                                                                                       present sequence
       22-JUL-2002;
13-AUG-2002;
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SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300 RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120 61 RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180 SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 1 MDPAGGPRGVLPRPCRVLVTLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA Gaps ; 87.5%; Score 336; DB 7; Length 384; 100.0%; Pred. No. 0; O; Mismatches 0; Indels RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKG 336 Query Match
Best Local Similarity 100.
Matches 336; Conservative Sequence 384 AA; 121 181 301 121 181 241 301 a g a g ò 셤 ઠે ઠ 셤 ò ઠ

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Gaps

63 77

(first entry)

20-MAY-2004

ADJ75441;

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ADJ75441 RESULT

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13. Also described: (l) a reagent (l) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent or the transpersion of the read bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease; (6) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a procein encoded by a marker gene; and (7) a DNA chip for testing for chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. The method in gene through an supering for a probe has been immobilised to assay a marker gene. The present for hydron-hial asthma or chronic obstructive pulmonary disease. The probent can antisense the probe has been immobilised to assay a marker gene. The present 64 VRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY 123 Testing for bronchial asthma or chronic obstructive pulmonary disease by bronchial asthma; chronic obstructive pulmonary disease; respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic; comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a 4 AGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHAREL 18 AGGPRGVLPRPCRVLVLINPRGGKGKALQLFRSHVQPLLAEABISFTLMLTERRNHAREL bronchial asthma or chronic obstructive pulmonary disease. The pr sequence is used in the exemplification of the present invention. ó, × Izuhara 86.7%; Score 333; DB 8; Length 398; 100.0%; Pred. No. 2.6e-317; ive 0; Mismatches 0; Indels Nagai H, Example 11; SEQ ID NO 693; 241pp; English. Kubo H, **Үатауа М**, 04-AUG-2003; 2003EP-00254857. 06-AUG-2002; 2002JP-00229312. 20-MAR-2003; 2003JP-00077212. Best Local Similarity 100. Matches 333; Conservative (GENO-) GENOX RES INC. Ohtani N, Sugita Y, gene therapy; marker WPI; 2004-193155/19. Sequence 398 AA; healthy subject. EP1394274-A2 Homo sapiens 03-MAR-2004. Query Match Best Local S ਨੇ 셤 ઠે ö This invention relates to a novel method of treating a human subject having a tumourigenic disorder or angiogenic disorder, caused by aberrant gene expression or activity of an isolated protein, by administering a modulator. The modulator may have cytostatic, antitipyroid, antidiabetic or ophthalmological activity. The method is useful for treating a subject having a tumourigenic or angiogenic disorder, in particular for treating cancer (for example breast cancer, colon cancer, lung cancer or prostatic cancer) and, for example, Grave's disease and diabetic retinopathy. The present sequence is the amino acid sequence of the novel isolated human 240 9 Treating subject having tumorigenic disorder or angiogenic disorder caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic acid, by administering a modulator. Lightcap ES; Lescon A, ADJ75441 standard; protein; 398 AA.

method for producing an animal model for bronchial asthma or chronic

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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are timulated with interleukin-13. Also described: (1) a resegent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
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                                     183
                                                         AGYEQVINEDLITINCTLILICRRILISPANILSLHTASGLRIFSVISLAWGFIADVDLESEK 197
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VRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
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                                                                                                                            PVPSHWTVVPDEDEFVLVLALLHSHLGSEMFAAPWGRCAAGVWHLFYVRAGVSRAMLLRLF
                                   AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEK
                                                                                                         YRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEE
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                                                                                                                                                                                                                                                                                                                                                                             ADJ75387 standard; protein; 398 AA
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20-MAR-2003; 2003JP-00077212.
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obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, amarker gene or an antisease nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polymucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; gene therapy; vaccine; SPHK1; EDG4; EDG8; tumour; cancer; pre-cancerous growth; colon cancer; ovarian cancer; lung cancer; breast cancer; rain cancer; bladder cancer; liver cancer; kidney cancer; head and neck cancer; stomach cancer; ocsophagus cancer; human; sphingosine kinase 1; enzyme.
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19-DEC-2002; 2002US-0434434P.
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 333; Conservative
                                                                                                                                                                                                                                                Sequence 398 AA;
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(TULA-) TULARIK INC

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Human sphingosine kinase (SK) partial fragment
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                          liver cancer
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Sphingolipid; cytostatic; gene therapy; cancer; sphingolipidose; SPL; sphingosine-1-phosphate lyase; sphingosine kinase; SK; enzyme; human.
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                                                                                                                                                                                                                                                                                                  The invention describes SPHK1, EDG4, EDG5, and EDG8 genes for diagnosing, treating, or preventing tumours and cancers in mammals. Also described are: diagnosing a cancer in a mammal, inhibiting cancer or pre-cancerous growth in a mammallan tissue; administering siRNA to a patient in need; clocking in vivo expression of a gene; screening a test molecule for blocking in vivo expression of a gene; screening a test molecule for SPHK1, EDG4, EDG5, or EDG8 antagonist activity; determining whether a test molecule has SPHK1, EDG4, EDG5, or EDG8 antagonist activity; cdetermining the efficacy of a therapeutic treatment regimen in a patient; conferming cancer or pre-cancerous growth in a mammalian tissue; agonists and inhibitors of SPHK1, EDG4, EDG5, or EDG8; and a pharmaceutical composition comprising the antibodies. The SPHK1, EDG4, EDG5, or EDG8, antibodies which specifically binds to SPHK1, EDG4, EDG5, or EDG8, and a pharmaceutical composition comprising the antibodies. The SPHK1, EDG4, EDG5, or EDG8 cancer, breast cancer, braid and neck cancer, braid and neck cancer, stomacr, or accer, head and neck cancer, stomach cancer, liver cancer. They can cancer, head and neck cancer, stomach cancer, or sophagus cancer. They can also be used as cancer vaccines. This is the amino acid sequence of human sphingosine kinase 1 (SPHK1).
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                                                                                                                                           Use of SPHK1, EDG4, EDG5, and EDG8 genes for diagnosing, treating, or preventing tumors and cancers in mammals, e.g. colon cancer, ovarian cancer, lung cancer, breast cancer, brain cancer, bladder cancer, or
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                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2; 176pp; English
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                                                                                                 N-PSDB; ADO22416, ADO22418
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                               Powers S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an agent that modulates sphingolipid metabolism for treating e.g., breast cancer by culturing a homozygous null mutant Drosophila melanogaster in the absence and presence of a candidate agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 NCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 VLVLLINPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 320; DB 6; Le
100.0%; Pred. No. 1.3e-304;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                          (CHIL-) CHILDRENS HOSPITAL & RES CENT AT OAKLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 125-126; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP71054 standard; protein; 384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYLVYVPVVAFRLEPKDGKG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2002; 2002US-00053510.
17-JAN-2002; 2002US-0349582P.
                                                                                                      17-JAN-2003; 2003WO-US001739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 320; Conservative
                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-663394/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                      Saba JD, Fyrst H;
                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ACF35857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 368 AA;
WO2003062390-A2
                                                      31-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ID ABP7
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ABP71054;

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factor (TNP)-induced cellular activity. The ended involves contacting the cell with an agent under conditions sufficient to modulate the interaction of sphingosine kinase with a TNF receptor-associated factor (TRAF), preferably TRAF2, where inducing the association up-regulates cellular activity, and inhibiting the association down-regulates cellular activity. The agent is useful for manufacturing a medicament for treating a mammal with a condition of aberrant, unwanted or inappropriate cytokine-induced cellular activity. The methods are useful for modulating cytokine-induced cellular activity. The methods are useful for treating or preventing a condition of aberrant, unwanted or inappropriate
                                                                                                                TINF; tummour necrosis factor; sphingosine kinase; TRAF; TRAF2; cytostatic; TNF receptor-associated factor; antiinflammatory; antirheumatic; human; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSIHTASGIRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating cytokine- or tumor necrosis factor-induced cellular activity, useful for treating or preventing a neoplastic condition, comprises modulating an intracellular sphingosine kinase-dependent signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to modulating cytokine-induced or tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine-induced or TNF-induced cellular activity in a mammal, such as neoplastic condition or inflammation (e.g. rheumatoid arthritis). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.7%; Score 287; DB 6; Length 384; 100.0%; Pred. No. 3.1e-272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents a human sphingosine kinase
                                                                                                                                                                                                                                                                                     379. .382
/note= "specifically claimed peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gamble J, Moretti P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                 /note= "Xaa is unknown"
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Fig 9; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2001; 2001AU-0000551.
13-AUG-2001; 2001AU-00006978.
27-DEC-2001; 2001AU-00009759.
                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-2002; 2002WO-AU000710
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEDV-) MEDVET SCI PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang L, Vadas M,
                                                                        Human sphingosine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity tou. Matches 287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-201282/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 384 AA;
                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                          WO200298458-A1
                                                                                                                                                                                           Homo sapiens
                                     14-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mechanism
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB80404-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune consents, autoimmune thyroiditis, diabetes mellitus, Crobn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                   181 SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                                                                                                                                                                                                                      antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 2585; 2081pp + Sequence Listing; English.
                                                                                287
                                                                                                       241 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.2%; Score 285; DB 5; Length 333; 100.0%; Pred. No. 2.4e-270; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                       ABB90209 standard; protein; 333 AA.
                                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 2585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-2000; 2000US-0205515P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2001; 2001WO-US016450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 74.2
Best Local Similarity 100.
Matches 285; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-122018/16.
N-PSDB; ABL90618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200190304-A2
                                                                                                                                                                                                                                                                                                       24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders.
                                                                                                                                                                                                                                                                 ABB90209;
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181
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immunosuppressant and cytostatic activity. The polynucleotides are useful

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180
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Zhang J, Zhao QA;
                                                                120
                                                                                    231
                                                                                                                                GPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVR 291
                                                                                                                                               GPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPWGRCAAGVWHLFYVR 240
                                         171
MLTERRNHARELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAG 111
                   9
                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Allahaimer's; Parkinson's disease; Huntington's disease; has amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
           SGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRILLSPMNLLSLHTASGLRLFSVLSLAW
                                                                                                  SGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAW
                                                                                     GFIADVDLESEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQ
                                                                                                                                                                                       AGVSRAMILRIPLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKG 336
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C, Asundi V, Chen R, Ma Y, (Wang Z, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 6897.
                                                                                                                                                                                                                                                          AAM41966 standard; protein; 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00598042.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-CCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00693036.
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                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153312-A1.
                                                                                                                                                                                                                                                                                                       22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                          leukaemia.
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Wang J, 1
Zhou P, (
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vel nucleic acids and polypeptides, useful for treating disorders such central nervous system injuries.

WPI; 2001-442253/47. N-PSDB; AA161122.

Novel

88

The invention relates to human nucleic acids (AAL57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,

Example 2; SEQ ID NO 6897; 10078pp; English.

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     in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, cancer disagnosis and therapy, drug screening, assays for receptor activity, are activity, and inflammation, leuksemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                        139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 VLALLHSHLGSEMFAAPMGRCAAGVWHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYL 319
                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDBDFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCT
                                                                                                                                                                                                                                                                                                                                         LLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLR
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                       Length 305;
                                                                                                                                                                                                                                                                                       0; Indels
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Pred. No. 6.3e-243;
                                                                                                                                                                                                                                               66.9%; Scor.
100.0%; Pred. No. v...
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 VYVPVVAFRLEPKDGKG 257
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 257; Conserv
                                                                                                                                                                                                                            Sequence 305 AA;
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OM protein - protein search, using sw model

June 15, 2005, 11:52:56 ; Search time 41 Seconds (without alignments) 901.152 Million cell updates/sec Run on:

US-10-642-289-2 2017 1 MDPAGGPRGVLPRPCRVLVL......CVEPPPSWKPQQMPPPEEPL 384 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description						hypothetical prote	conserved hypothet	conserved hypothet		hypothetical prote	conserved hypothet	transcription regu	transcription regu	hypothetical prote	œ		hypothetical prote	conserved hypothet	hypothetical prote		conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	multidrug resistan	probable ATP-depen
	ID	T05162	T19707	S51398	T38776	867059	T33517	AH1769	AE1394	H69995	A83894	F69795	D86677	F86849	AG1665	F83871	F84898	AI1293	AH1528	AB2166	AF1171	G95120	H70861	C97990	C70596	A89978	D83734	F72386	F69595	E72611
	8	0	~	~	7	~	~	~	7	~	~	7	~	~	~	7	7	7	7	7	~	0	~	7	~	~	~	~	~	N
	Match Length		473	687	458	624	549	306	306	309	295	303	342	302	310	311	364	310	309	315	309	294	309	311	321	315	295	304	297	1273
* Query	Match	22.3	18.6	17.7	17.6	17.2	12.3	7.7	6.9	6.8	6.5	6.4	6.3	6.2	6.2	6.1	6.1	9	5.9	5.8	5.6	5.5	5.5		5.5	5.3	5.2	5.5	5.1	5.1
	Score	449	375.5	357.5	355	346	247.5	154.5	139.5	136.5	131	129.5	127	126	125.5	122.5	122.5	120.5	118	117	113	111	111	111	111	106	105.5	104	102	102
Result	No.		7	e	4	S	ø	7	8	6	10	11	12	13	14	15	16	17	18	19	70	21	22	23	24	25	26	27	28	53

		hypothetical prote	conserved hypothet	gene retII protein	diacylglycerol kin	diacylglycerol kin	semaphorin C - mou	hypothetical prote	conserved hypothet	probable diacylgly	probable hydrolase	probable aminoadip	hypothetical prote	hypothetical prote	conserved hypothet
875948	C83634	G89844	D75405	138153	A46140	B46140	148746	T16422	A86842	H84567	AE0724	T41029	T17255	A97482	AI2699
7	N	~	~	N	N	~	~	~	~	~	~	~	7	~	~
433	449	305	311	899	791	196	782	732	304	475	219	981	1192	325	325
٥.	4.9	4.8	4.8	4.7	4.6	4.6	4.6	4.6	4.5	4.5	4.5	4.5	5.5	4.5	4.5
S															
100.5 5	66	97.5	97	94	93.5	93.5	93	92.5	91.5	91.5	91	91	91	90.5	90.5

## ALIGNMENTS

	RESULT 1 TO1162 TO01162 TO01162 C;Species: Arabidopsis tha C;Date: 23-Apr-1999 #seque: C;Accession: T05162 C;Accession: T05162 R;Bevan, M.; Peters, S.A.; submitted to the Protein S.A;Accession: T05162 A;Accession: T05162 A;Accession: T05162 A;Molecule type: DNA A;Residues: 1-1240 <bev> A;Cross-references: UNIPRO A;Axperimental source: cul C;Genetics:</bev>	RESULT 1 T05162 Tyour 1 T05162 Tyour 1
<u> </u>	A; Map position: A; Introns: 44/3 A; Note: F18E5.1	A;Map position: 4 A;Introns: 44/3; 117/3; 178/3; 206/1; 237/2; 375/1; 416/1; 449/3; 474/1; 503/1; 529/1; 5: A;Note: F18E5.160
	Query Match Best Local Si Matches 122;	Query Match 22.3%; Score 449; DB 2; Length 1240; Best Local Similarity 31.9%; Pred. No. 2.2e-31; Matches 122; Conservative 63; Mismatches 127; Indels 70; Gaps 13;
	Oy 11 I Db 374 I	11 LPRPCRVLVLINPRGGKGKALQLFRSHVQPLLABABISFTLMLTERRNHARELVRSEELG 70
	Oy 71 F	71 RWDALVVMSGDGLMHEVVNGLMERFDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVT 130 ::  :  :        ::
	Oy 131 N	131 NEDLLTNCTLLICRRILSPNNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEM 190 
_	Qy 191 F	191 RFTLGTFL
	Oy 231 -	231QGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHS-HLGSE-MFA 274
	Oy 275 1 Db 654 1	275 APMGRCAAGVMHLFYVRAGVSRAMILRLFIAMEKGRHWEYECPYLVYVPVVAFRL 329 
	Oy 330 I	330 EPKDGKGMFAVDGELM 345 

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11;

Gaps

81;

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A;Cross-references: UNIPROT:014159; EMBL:298762; PIDN:CAB11477.1; GSPDB:GN00066; SPDB:SP?
A;Experimental source: strain 972h-; cosmid c4A8
                                                                                382 SYSTLCLIKSIETRIDLMCCSQPSYAREHPKLSFLSQTYGLIAETDINTEFIRWMGPARF 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 VMSGDGLMHEVVNGLMERPDWETAIQK-PLCSLPAGSGNALAASLNHYAGYEQVTNEDLL 135
                                                                                                                                                                                                  TNCTLLLCRRLLSPMNLLSLHTASGLR---LFSVLSLAWGFIADVDLESEKYRRLGEMRF 192
                                                                                                                                                                                                                                                                                                                                              ----- RGRLAYLPV----- 215
                                                                                                                                                                                                                                                                                                                                                                                       442 ELGVAFNIJOKKKYPCEIYVKYAAKSKNELKNHYLEHKNKGSLEFOHITMNKDNEDCDNY 501
                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GRVGSKTPASPVVVQQGPVDAHLV--------PLEEPVPSHWTV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 VPDEDFVLVLALLHS----HLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAME 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEDLLTNCTLLLCRRLLSPMNL-LSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 MRFTLGTFLRL------AALRT----YRGRLAYLPVGRVGSKTPASPVVV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SPAC4A8.07c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KPALTALEILKGR----PTSFDLMTFEQKGKKAYSFLTANYGIJADCDIGTENWRFMGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 KGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHP 356
  Length 687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.6%; Score 355; DB 2; Length 45
29.5%; Pred. No. 1.4e-23;
tive 64; Mismatches 144; Indels
                                          Indels
Query Match 17.7%; Score 357.5; DB 2; Best Local Similarity 24.9%; Pred. No. 1.4e-23; Matches 102; Conservative 76; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                              TLGTFLRLAALRTY-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 109; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: SPDB: SPAC4A8.07c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-458 <SKE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 1
A;Introns: 39/1; 101/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: T38776
                                                                                                                                                                                                                                                            136
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                                                                                                                                                                                                                                                                                                                                                 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
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                                                                                                      submitted to the EMBL Data Library, October 1995
A;Reference number: Z19167
A;Accession: T19707
A;Status preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-473 <WIL>
A;Cross-references: UNIPROT:018425; EMBL:Z66494; PIDN:CAA91259.1; GSPDB:GN00020; CESP:C3
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q06147; EMBL:U17244; NID:g577171; PIDN:AAB67377.1; PID:g5771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 KVKTNGSVSDSEEETMETKPQNWTLPDSDETLAVGSSDLEETVVIEDNFVNIYAVTLSHI 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: || : : || : : || : : || 376 AADGPFAPSAKLEDNRIHLSYILWKDIGTRVNIAKYLLAIEHETHL--DLPFVKHVEVSS 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 GYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHT--ASGLRLFSVLSLAWGFIADVDLESE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYRR-LGEMRFTLGTFLRLAALRTYRGRLAYLP------VGRVGSKTPASPV--- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TVVPDEDFVLVLALLHSHL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 SEELGRWDALVVMSGDGLMHEVVNGLMERPD-WETAIQKPLCSLPAGSGNALAASLNHYA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 GSEMFAAPMGRCAAGVMHLFYV -- RAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YLR260w - yeast (Saccharomyces cerevisiae)
N,Alternate names: hypothetical protein L8479.7
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S51398
R;Miller, N.
submitted to the EMBL Data Library, November 1994
A;Description: The sequence of S. cerevisiae cosmid 8479.
A;Reference number: S51398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 PRP---CR--VLVLLNPRGGKGKALQLFRSHVQPLLABAEISFTLMLTERRNHARE-LVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%; Score 375.5; DB 2; Length 28.6%; Pred. No. 2.1e-25; ative 80; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                A;Map position: 2
A;Introns: 82/1; 126/1; 158/3; 276/1; 311/3; 427/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| : :: :: :: WKLEVISEGSHVVLDGEVVDTKTIE 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRLEPKDGKGMFAVDGELMVSEAVQ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 -VVQQGPVDAHLVPLEEPVPSHW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: SGD:LCB5; MIPS:YLR260w
A,Cross-references: SGD:S0004250
A,Map position: 12R
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.64
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-687 <MIL>
                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP: C34C6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327
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submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid T10B11.
A;Reference number: Z21363
A;Accession: T3517
A;Accession: T3517
A;Aclatus: preliminary; translated from GB/EMBL/DDBJ
A;Roldues: 15-59 <MIN>
A;Residues: 15-59 <MIN>
A;Residues: USPS: T15-59 <MIN>
A;Residues: UNIRROT: OgrZI1; EMBL: AF098993; FIDN: AAC67466.1; GSPDB: GN00019; CESP: T3 A;Reperimental source: strain Bristol N2; clone T10B11
A;Gross-references: UNIRROT: OgrZI1.
A;App position: 1
A;App position: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Accession: All769
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, S; C, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A, Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A, Fittle: Comparative genomics of Listeria species.
A, Fittle: Comparative genomics of Listeria species.
A, Feference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIFROT:Q927T6; GB:AL592022; PIDN:CAC97928.1; PID:g16415238; GSPDB:GPA;Experimental source: strain Clipl1262
C;Genetics:
A;Gene: lin2702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |:: :::: | | : : | | : : | | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 VGSKTPASPVVVQQGPVDAHLVPLEEPVP-----SHW-----TVV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 LSHKENVNP-----KDQLPPCLEPCPVCMKPQGNDKYDYHWHAEFTHVICCVIPTVT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 PDEDFVLVLALLHSHLGSEMPAAPMGRCAAGVMHLFYV-RAGVSRAMLLRLFLAMEKGRH 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 PRTPYGL-------APFTGIGDGTLDLALVPRISRFHNMQFMRKVAMYGGKQ 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 MEYECPYLVYVPVVAFRLEP---KDGKGMFAVDGELM---VSEAVQGQVHP---NYFWMV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGNALAASLNHYAGYEQVTNED------LLTNCTLLLCRRLLSPMNLLSLHTASGLRL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 26/1; 76/2; 109/3; 159/1; 187/3; 229/3; 353/1; 398/2; 434/1; 467/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 FSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRT-----YRGRLAYLPVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 RGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLL-AEAEISFTLMLTERRNHARBLVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EELGRW----DALVVMSGDGLMHEVVNGLMERPDWETA--IOKPLCSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%; Score 247.5; DB 2; 23.5%; Pred. No. 6.5e-14; tive 72; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.3
Best Local Similarity 23.5
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |:|
528 AAMVKP 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: AH1769
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-306 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
867059
hypothetical protein YOR171c - yeast (Saccharomyces cerevisiae)
hypothetical protein 03615
C;Species: Saccharomyces cerevisiae
S;Species: Saccharomyces cerevisiae
S;Species: Saccharomyces cerevisiae
R;Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Winsc submitted to the Protein Sequence Database, July 1996
A;Reference number: S6703
A;Reference number: S6703
A;Molecule type: DNA
A;Molecule type: DNA
A;Residucule type: 1624 cBOR>
A;Cross-references: UNIPROT: Q12246; EMBL: Z75078; NID: g1420415; PID: g1420417; GSPDB: GN000
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 NLGVAFNIIQGKKYPCEVFVKYAAKSKKELKVHFLENKDKNKGCLTFEP-----NPSPNS 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VPLEEPVPSHWTVVPDEDFVLVLALLHS- 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPDILSKANINNSTKDELSPNFLNEDNFKLKYPMTEPVPRDWEKM-DSELTDNLTIFYTG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 VMSGDGLMHEVVNGLMERPDWETALQK-PLCSLPAGSGNALAASLNHYAGYEQVTNEDLL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INCTLLLCRRLLSPMNLLSLHTASGLR---LFSVLSLAWGFIADVDLESEKYRRLGEMRF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 TLG------TPLRLAA----LRTY-----RGRLAYLPVGRVGSKTP-A 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---HLGSEMFAAPMGRCAAGVWHLFYVRAGVSRAMLLRLFLAMBKGRHMEYECPYLVYVP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFY 289
                                                                                                                                                                                                           290 VRAGVSRAMILRLFLAMEKGRHMEYECPYLVYVPVVAFRLEP-KDGK-GMFAVDGELMVS 347
                                                                                                                                                                                                                                                                --INDLSIFCAGLLPYIAPDAKMFPAASNDDGLIDVVI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 VLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypochetical protein T10B11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dete: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 09-Jul-2004
C;Accession: T33517
R;Minx, P:; Kemp, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYAALCLVKSIETRIDLMCCSQPSYMNEWPRLSPLSQTYGVIAESDINTEFIRWMGPVRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 346; DB 2; Length 624; Pred. No. 1.3e-22; 82; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHP 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.2%;
25.7%;
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A,Cross-references: SGD:S0005697
A,Map position: 15R
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Best Local Similarity 25.79
Matches 101; Conservative
                                                                                                                                327 STSP-ESHLLTFE-
                                                                                                                                                                                                                                                                                                                                                                                            EAVOGOVHP 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 EPPECRVAP 441
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Qy 251 VVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAM 306	RESULT 9  RESULT 9  RESULT 9  REPACES 19 TO THE SEALILES SUBLISS SUBLISS  C. Stores: 0-Dec-1997 HEAVE, Change 09-Jul-2004  C. Accession: H6993  R. KANDEL, F.; Decaration, C.; Abbettin, A. M.; Alloni, G.; Aberedo, V.; Berter  R. KANDEL, F.; Decaration, F.; Bruchl, C.V.; Caldwall, B.; Capuano, V.; Carrer, N. M.; Chol  A.; BELLIAL, S. O.S. Emmano, F.T.; Billari, K.D.; Fairington, J., Tabret, C.; Perrari, E.  A.ANDEDORE: A. D. S. Emmano, F.T.; Billari, K.D.; Fairington, J., Tabret, C.; Perrari, E.  A.ANDEDORE: A. S. O.S. Emmano, F.T.; Billari, K.D.; Fairington, J., Tabret, S.; Hallon, M.F.;  KONCHER, P.; KONINGSER, D.; PITTS, C. Projita, M.; Pujita, K.; Puma, S.; Gallari, M.; Alabber, J.; Harrow, V.; Pallare, M.; Mallare, J.; Hosono, M.; Maneal, A.; Marchor, S.; Maneal, S.; Maneal, A. M.; Order, E.; Roche, E.; Roche, R.; Sandan, S.; Maneal, S.; Maneal, A. M.; Order, E.; Roche, E.; Roche, R.; Sandan, S.; Maneal, S.; Manea	
Query Match 7.7%; Score 154.5; DB 2; Length 306; Best Local Similarity 22.2%; Pred. No. 5.7e-06; Matches 77; Conservative 66; Mismatches 129; Indels 75; Gaps 16; Qy 16 RVLVLLNPRGGKCKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWD 73 :::	0y 11 NEPLLTWORTHERPOWGLAGEREPONETRICKELFAGGRALANGIANTOATENT 130  0y 113 NEPLLTWORTLICERLESPONTISH	

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                                                            Query Match
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   A,Gene: yerQ
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Matches
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F69795
Conserved hypothetical protein yerQ - Bacillus subtilis
CiSpeciaes: Bacillus subtilis
CiAccession: F69795
R.Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Eron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laululo, M.F.
Koetter, P.; Koningstein, G.; Rrogh, S.; Kumano, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Munters, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Hunters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A.; Litle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A.; Althors: Aseriae Rose, M.; Mulder, A.; Mulder,
   C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C; Accession: A83894
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Accession: A83894
A; Status: preliminary
A; A; Catus: preliminary
A; Residues: 1-295 < CTO>
A; Residues: 1-295 < CTO>
A; Cross-references: UNIPOT:Q9KBH4; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB056
                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9KBH4; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB056 A;Experimental source: strain C-125 C;Genetics: A;Gene: BH1953
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A;Experimental source: strain 168
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GGDGTINEVANGLVNH------RVPLGIIPAGSGNDFARCLNIPMHYEKALHR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ---IPENKQKKVDLLHLGQRHCLTVTGI-----GFDGKIAKTVNEAIYKNWFNQFGFGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 EKGRH--MEYECPYL----VYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQV 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.5%; Score 131; DB 2; Length 29
22.0%; Pred. No. 0.00067;
:ive 50; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 SYVLS---MLEVLKDYR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 22.0%
Matches 78; Conservative
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transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403) (Species: Lactococcus lactis subsp. lactis subsp. lactis c.5secies: Lactococcus lactis subsp. lactis c.5cession: Lactococcus lactis subsp. lactis c.5decession: D86677
R;Bolotin, A.; Winoker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res II, 731-753, 2001
A;Itle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg. A;Accession: D86677
A;Ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 NEDLLTNCTLLLCRRLLSPWNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------KPLEAIEI-----1GKNQILNIDVGHAVIRETQDEQY----- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----- 174
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                                                                                                                                                                                                                                                                                                                                                                            DALVVMSGDGLMHEVVNGLM---ERPDWETAIQKPLCSLPAGSGNALAASINHYAGYEQV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNEDLLINCTLLLCRRLLSPWNL-----LSLHTASGLRLFSVLSLAWGFIADVDLESEK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
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                                                                                                                                                                                 16 RVLVLLNPRGGKGKALQLFRSHVQPLL---AEAEISFTLMLTERRNHARELVRSEELGRW 72
                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 YRRLGEMRFTLGTFLRLAALR-----TYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VLVLALLHSHLGSEMFAAPM
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                                                                                                                                                                                                                                                 6.3%; Score 127; DB 2; Length 342;
20.7%; Pred. No. 0.0019;
tive 54; Mismatches 122; Indels 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 KTMLGQLAYYLKGMEMLPSLRPTEVEIEYDGKLF------
6.4%; Score 129.5; DB 2;
20.6%; Pred. No. 0.00094;
tive 44; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----HIIYTKANRVKVNVSEKMQLNL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 GRCAAGVMHLFY----VRAGVSRAMLLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:09CIE3; (A;Experimental source: strain IL1403 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 LVPLEEPVPSHWTVVPDEDF-
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                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 73; Conserva
                                                           Similarity
68; Conserv
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DB 2; Length 310;

55; Mismatches 118;

.0022;

6.2%; Score 125.5; 21.3%; Pred. No. 0.0

21.3%;

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C'Accession: F83871

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c A;Reference number: A83650; MUID:20512582; PMID:11058132
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A;Cross-references: UNIPROT:Q9KC00; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB0545
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multidrug resistance protein bmrU [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 RWDALVVWSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 NEDLLITNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKY----- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----RALHVPRDV-----IKATKIIAAGQSVAMDIGKANDTYFINIGG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 -RRIGEMRFTLGTFLRLAALRTYRGRLAY-----LPVGRVGSKTPASPVVVQQGPVDA 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VFEGEVMFFLLGLTNSIGGFEKI-APDAKLDDGKFSLIIVKK-VNL 230
                                                                                                                                                                                                                                                                                                                          19 VLLNPRGGKGKALQLFRSHVQPLLAEAE-----ISFTLMLTERRNHARELVRSEELG 70
                                                                                                                                                                                                                                                                                                                                                                            |: || || : : : : : : : || || || || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 AMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGEL
A, Experimental source: strain Clip11262 C, Genetics:
                                                                                                                                                                                                                                           74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Conservative
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: F83871
                                                                                  A;Gene: lin1865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
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                                                                                                                                                                                                                                                                                         transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 C; Accession: F86849 R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001 A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A; Accession: F86649 A; Edatus: preliminary A; Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Residues: 1-302 <STO>
A,Cross-references: UNIPROT:Q9CEN8; GB:AE005176; PID:g12724823; PIDN:AAK05896.1; GSPDB:G
A,Experimental source: strain IL1403
C,Genetics:
A,Gene: ysfG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 INHEIFIMN-------YQSKGLSGYALNNIGIGLDATI-VKSANEGKLK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL------NHYAGYEQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 IIGGDGTISLVINELPE-----EEAFSYIPSGSGNDFARSLKLKLDPIESFEAARRG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EM--RFILGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: : | | : | | : : | OVLNKLKLGSF-----SYI-----LTALHVLITKKPFPA-LIEVEN--- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---QEISLENAFLMTFTKHPYFGGGVKISPEATNENADIHL----VEYNKHHLLRTFSLI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VINEDLLINCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 SHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFL-- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 VLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRS--EELGRWDALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 -AMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQ--GQVH 355
                                             AGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDG-KGMFAVDGE 343
                                                                                           : |: | : |: | : | : | | TD-NLFELIALLAIVANGKHL--DDVNLEYIKTSKIEIEALGGQKILLNLDGE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.2%; Score 126; DB 2; Length 302;
21.2%; Pred. No. 0.0019;
tive 64; Mismatches 123; Indels
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nes 75; Conserv
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RESULT 14
AG1665
hypothetical protein homolog lin1865 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: Dominguez-Bernal, G; Duchaud, E; Durand, L; Dussurget, O; Entian, K.D.; Fsihi, H.D.; Jones, L.J.; Kuhn, M.; Kunst, F.; Kurapkat, G; Madueno, E; Maitournam, A; Machiners: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G; Madueno, E; Maitournam, A; Machiners: Reft, J; Sinnoes, N.; Teierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Ttle: Comparative genomics of Listeria species
A;Ttle: Comparative genomics of Listeria species
A;Actession: AG1665
```

A, Cross-references: UNIPROT: 092A05; GB: AL592022; PIDN: CAC97095.1; PID: 916414366; GSPDB: d

Search completed: June 15, 2005, 12:03:16 Job time : 43 secs g

'n

Gaps

6

DB 2; Length 311;

6.1%; Score 122.5; DB; 30.5%; Pred. No. 0.0041;

17; Mismatches

5

16 RVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDAL 75

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76 VVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein June 15, 2005, 12:02:38; Search time 157 Seconds (without alignments) 937.582 Million cell updates/sec Run on:

Title:

US-10-642-289-2 2017 1 MDPAGGPRGVLPRPCRVLVL.......CVBPPPSWKPQQMPPPEEPL 384

Perfect score: Sequence:

Scoring table:

1710399 segs, 383334425 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:\*

| cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
5: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
6: /cgn2\_6/ptodata/1/pubpaa/US07\_BWB\_PUB.pep:\*
7: /cgn2\_6/ptodata/1/pubpaa/US09\_WEW\_PUB.pep:\*
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16: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
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19: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
20: /cgn2\_6/ptodata/1/pubpaa/US11\_WEW\_PUB.pep:\*
21: /cgn2\_6/ptodata/1/pubpaa/US11\_WEW\_PUB.pep:\*
22: /cgn2\_6/ptodata/1/pubpaa/US11\_WEW\_PUB.pep:\*
22: /cgn2\_6/ptodata/1/pubpaa/US11\_WEW\_PUB.pep:\*
23: /cgn2\_6/ptodata/1/pubpaa/US11\_WEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:

#### SUMMARIES

Result No.	Score	& Query Match	% Query Match Length DB ID	DB	a	Description
	2017	!	!	16	US-10-642-289-2	Sequence 2, Appli
7	2013			Q	US-09-970-516-2	Sequence 2, Appli
n	2013			14	US-10-354-358-26	Sequence 26, Appl
4	2013			15	US-10-619-344-2	Sequence 2, Appli
'n	2005			σ	US-09-796-487-3	Seguence 3, Appli
9	2005			16	US-10-723-860-722	Sequence 722, App
7	2004			17	US-10-479-933-1	Sequence 1, Appli
80	1996			16	US-10-715-117-2	Sequence 2, Appli
0	1959	97.1	384	6	US-09-784-810A-2	Sequence 2, Appli
10	1920			14	US-10-053-510-21	Sequence 21, Appl
11	1920			15	US-10-348-052-21	Sequence 21, Appl

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Gaps

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2-01 4-23 -810 -516 -676	US-09-796-487-2 US-10-830-677-15 US-09-796-487-1 US-09-796-487-4 US-09-796-487-5 US-09-933-767-32	14 US-10-004-860-328 14 US-10-023-282-328 0 US-09-796-487-9 9 US-09-817-676A-12 16 US-10-830-677-12 9 US-09-817-676A-14	US-09-970-516-4 US-10-354-358-7 US-10-830-677-4 US-10-737-450-1 US-09-969-896-3 US-10-631-958-3	14 US-10-053-510-19 15 US-10-348-052-19 16 US-10-622-011-19 15 US-10-622-011-28 16 US-10-053-510-20 14 US-10-053-510-20 15 US-10-348-052-20 16 US-10-348-052-20
382238	388 388 381 373 293	293 293 204 617 618	618 618 618 618 638	6 4 4 9 0 4 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0
95.2 86.7 81.1 80.8 80.8	80.7 80.5 80.5 79.6 76.3	76.3 44.4 4.4.3 3.3 8.3	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	27.8 27.8 27.8 27.8 22.7.8 25.8 25.8
1920 1749 1636.5 1629.5 1629.5		1538 1538 935.5 894 894 893	883.5 883.5 883.5 883.5 833.5 830.5 830.5	560 560 560 560 519 519 519 519
12 13 14 15 17	18 19 20 22 23	22222 2225 2327 298	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	C C C C C C C C C C C C C C C C C C C

#### ALIGNMENTS

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Query Match

100.0%; Score 2017; DB 16; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 384; Conservative 0; Mismatches 0; Indels 0;
     US-1U-642-289

US-1U-642-289

Publication No. US20040132053A1

GENERAL INFORMATION:

APPLICANT: PITSON, SLUETT M

APPLICANT: PITSON, WATTENBERG W

APPLICANT: PITAGON, WATTENBERG W

APPLICANT: PITAGON, STENATE B

APPLICANT: Wathew, VADAS A

TITLE OF INVENTION: SPHINGOSINE KINASE ENZYME

FILE REFRENCE: PITSON=1

CURRENT APPLICATION NUMBER: US/09/959, 897

PRIOR PILING DATE: 2003-08-18

PRIOR FILING DATE: 2003-08-18

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

SOFFWARE: PATCHTING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 56

SOFFWARE: PATCHTING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 56

LENOTH: 384

TUBNOT: PATCHTING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Homo sapiens
US-10-642-289-2
US-10-642-289-2
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RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW 360
                                                                                                361 MVSGCVEPPPSWKPQQMPPPEEPL 384
                                                                       361 MVSGCVEPPSWKPQQMPPPEEPL 384
                                                                                                                                                                                                   Sequence 26, Application US/10354358 Publication No. US20030157082A1 GENERAL INFORMATION:
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Best Local Similarity 99.7
Matches 383; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                      US-10-354-358-26
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APPLICANT: No. US20020099029Alartis AG
APPLICANT: No. US20020099029Alartis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-316.7
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
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                                                                                                            61 RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
                                                                                                                                                                    NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                        121 NHYAGYEQVINEDLLINCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAMGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                      LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
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                                   MDPAGGPRGVLPRPCRVLVILNPRGGKGKALQIFRSHVQPLLAEAEISFTLMLTERRNHA 60
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US-09-970-516-2
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LENGTH: 384
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| APPLICANT: MILERINUM PLATMACCULICALS, INC. |
| APPLICANT: MILERINUM PLATMACCULICALS: MILERINUM PLATMACCULICALS: MILERINUM PLATMACCULICANT: MAILERY, Obn. JOSCPH
| APPLICANT: Halls | Fong-Ying |
| APPLICANT: Lescon, Andrea |
| APPLICANT: Lescon, Andrea |
| APPLICANT: Milliamson, Mark |
| TITLE OF INVENTION: 1781 |
| TITLE OF INVE
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61 RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
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FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(384)
OTHER INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, corresponters in INFORMATION: adding to amino acid residue 1 to 384 of Homo sapiens SPHK-1 of GeOTHER INFORMATION: name sequence Accession Number AAF73423.
FUBLICATION INFORMATION:
AUTHORS: Nava et al.
TITLE: Functional characterization of human spingosine kinase-1
                                                                                                                                             APPLICANT: Spiegel. Sarah
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REPERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Version 3.1
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99.0%; Pred. No. 1.8e-188;
tive 3; Mismatches 1;
361 MVSGCVEPPSWKPQQMPPPEEPL 384
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DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1).. (384)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AFF73423
DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1).. (384)
                                                                                        ; Sequence 3, Application US/09796487; Patent No. US20020042358A1; GENERAL INFORMATION:
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Best Local Similarity 99.0°
Matches 380; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ISSUE: 1
PAGES: 81-84
DATE: 2000
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US-09-796-487-3
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| Sequence 2, Application US/10619344
| Publication No. US20040086487A1
| GENERAL INFORMATION:
| APPLICANT: Novartis AG
| TITLE OF INVENTION: Induction of blood vessel formation through administration of
| TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
| FILE REPERENCE: 4-3167 |
| CURRENT APPLICATION NUMBER: US/10/619,344 |
| CURRENT PILING DATE: 2003-07-14 |
| PRIOR APPLICATION NUMBER: US/09/970,516 |
| PRIOR FILING DATE: 2001-10-04
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                                                                                                  SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
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Pred. No. 2.9e-189;
1; Mismatches 0;
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Best Local Similarity 99.7%;
Matches 383; Conservative
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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LENGTH: 384
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Matches 381; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                         NAME/KEY: VARIANT LOCATION: 354
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US-10-715-117-2
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                                                               US-10-723-860-722

JSGQUENCE 722, Application US/10723860

Sequence 722, Application US/10723860

PUDLICACION NO. US2004025366A1

GENERAL INFORMATION:
APPLICANT: Aliz, Matasha

JAPPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert

JITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions FILE REPERENCE: 05882.0193 NPUS01

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT FILING DATE: 2003-11-26

PRIOR PILING DATE: 2003-11-26

NUMBER OF SEQ ID NOS: 8993

SOFTWARR: Patentin version 3.2

SEQ ID NO 722
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Pred. No. 1.8e-188;
3; Mismatches 1;
                361 MVSGCVEPPPSWKPQQMPPPEEPL 384
MVSGCVEPPSWKPQQMPPPEEPL 384
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Sequence 1, Application US/10479933
GENERAL INFORMATION:
APPLICANT: Xia, Pu
APPLICANT: Wang, Lijun
APPLICANT: Wadas, Mathew
APPLICANT: Gamble, Jennifer
APPLICANT: Moretti, Paul
APPLICANT: Pitson, Stuart
APPLICANT: Pitson, Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                  99.4%;
99.0%;
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Best Local Similarity 99.0
Matches 380; Conservative
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/ ORGANISM: Homo sapiens

US-10-723-860-722
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61 RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
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TITLE OF INVENTION: SPHINGOSINE KINASE INTERACTS WITH TRAF2 AND
TITLE OF INVENTION: MODULATES TUMOR NECROSIS FACTOR-INDUCED CELLULAR
TITLE OF INVENTION: ACTIVITY
FILE REPERRNCE: 650063.40140FC
CURRENT APPLICATION NUMBER: US/10/479,933
CURRENT FILING DATE: 2003-12-05
PRIOR APPLICATION NUMBER: PCT/AU02/00710
PRIOR FILING DATE: 2002-06-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1: 384
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; Sequence 2, Application No. U220040171037A1
; Publication No. U220040171037A1
; GENERAL INFORMATION:
; APPLICANT: LI, JING
; APPLICANT: SIN, WUN CHEY
; APPLICANT: SIN, WUN CHEY
; APPLICANT: YANG, JIANXIN
; TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
; FILE REFERENCE: 38002-0062
; CURRENT FILING AATE: 2003-11-18
; PRIOR APPLICATION NUMBER: 60/427,202
; PRIOR PLILING DATE: 2002-11-19
; PRIOR FILING DATE: 2002-11-19
; PRIOR FILING DATE: 2002-11-19
; WUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver: 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.2%; Score 2004; DB 17; 99.2%; Pred. No. 2.2e-188;
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US-10-479-933-1
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241 FVLVIALLHSHLGSENPAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYEC 300
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                   SEKYRRIGEMRPTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Saba, Julie D.
APPLICANT: Saba, Julie D.
APPLICANT: Fyrst, Henrik
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: POLYNUCLECTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 200116.402C2
CURRENT APPLICATION NUMBER: US/10/053,510
CURRENT FILIN DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASELSEQ for Mindows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 21, Application US/10053510; Publication No. US20030175939A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 2, Application US/09784810A

Patent No. US20020082203A1

GENERAL INFORMATION:

APPLICANT: RASTELL! LUCA

TITLE OF INVENTION: SAME

TITLE OF INVENTION: SAME

FILE REPRENCE: 10716-08

CURRENT APPLICATION NUMBER: US/09/784,810A

CURRENT APPLICATION NUMBER: 60/182,360

PRIOR APPLICATION NUMBER: 60/182,360

PRIOR APPLICATION NUMBER: 60/181,261

PRIOR APPLICATION NUMBER: 60/191,261

PRIOR PILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 2

LENGTH: 384
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                                                                                           Length 398;
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                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1996; DB 16;
Pred. No. 1.4e-187;
1; Mismatches 0;
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                                                                                          99.0%;
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Best Local Similarity 97.4
Matches 374; Conservative
                                                                                                                             Matches 383; Conservative
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US-09-784-810A-2
                        TYPE: PRT
CRGANISM: Homo sapiens
US-10-715-117-2
                                                                                          Query Match
Best Local Similarity
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US-09-784-810A-2
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          Sequence 21, Application US/10348052
| Publication No. US20030219782A1
| GENREAL INFORMATION:
| APPLICANT: Fyrst, Henrik
| TITLE OF INVENTION: OF SPHINGOLIPID METHODS FOR THE MODULATION
| TITLE OF INVENTION: OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
| FILE REFERENCE: 200116.405
| CURRENT FILING DATE: 2003-01-17
| NUMBER OF SEQ ID NOS: 29
| SOFTWARE: PastSEQ for Windows Version 4.0
| LENGTH: 368
| TYPE: RRT
| CORGANISM: Homo sapiens
| US-10-348-052-21
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
TITLE OF INVENTION: OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
FILTE OF INVENTION: OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
FILTE OF INVENTION: 0.002.4011
CURRENT APPLICATION NUMBER: US/10/622,011
CURRENT FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 368
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Pred. No. 3.9e-180;
1; Mismatches 0;
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Sequence 21, Application US/10622011

Publication No. US20040126834A1

GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-622-011-21
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US-10-348-052-21
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Sequence 2589, Application US/10264237

Publication No. US20040009491A1

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAIJ1P1

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 2585
Score 1920; DB 16; Length 368; Pred. No. 3.9e-180; 1; Mismatches 0; Indels 0
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99.7%; Pred. No. 2.4e-163;
iive 1; Mismatches 0;
      Query Match
Best Local Similarity 99.7%;
Matches 367; Conservative
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Best Local Similarity 99.7'
Matches 332; Conservative
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; ORGANISM: Homo sapiens
US-10-264-237-2585
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GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT APPLICATION NUMBER: 00/102-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENT NOS: 29
SOFTWARE: PATENT NO 4
TOWN OF A TOWN OF TO
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241 AGVSRAMLIRIFILIMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQ 300
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80.7%; Pred. No. 3.5e-152;
ive 34; Mismatches 39; Indels
                                                                                                                                                                                        MVCGSRDAPSGRDSRRGPPPEEP 382
                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09784810A
Patent No. US20020082203A1
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Best Local Similarity 80.7%
Matches 309; Conservative
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US-09-784-810A-4
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Sequence 6, Application US/09970516 Patent No. US20020099029A1 GENERAL INFORMATION:

US-09-970-516-6

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           formation through administration sphingosine kinases
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                                                                                                                                                                                                                                                                   Length 382;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                   80.8%; Score 1629.5; DB 9;
80.4%; Pred. No. 1.7e-151;
tive 34; Mismatches 40;
           TITLE OF INVENTION: Induction of blood vessel TITLE OF INVENTION: polynucleotides encoding FILE REPRENCE: 4-31617 CURRENT APPLICATION NUMBER: US/09/970,516 CURRENT FILING DATE: 2001-10-04 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin version 3.1 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MVSGCVEPPSWKPQQMPPPEEP 383
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APPLICANT: No. US20020099029Alartis AG
                                                                                                                                                                                                                                                                                           Best Local Similarity ...-
Matches 308; Conservative
                                                                                                                                                                                           TYPE: PRT
CORGANISM: Mus musculus
US-09-970-516-6
                                                                                                                                                                                                                                                                                         Similarity
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein June 15, 2005, 11:52:11 ; Search time 163 Seconds (without alignments) 911.141 Million cell updates/sec Run on:

US-10-642-289-2 2017 1 MDPAGGPRGVLPRPCRVLVL......CVEPPPSWKPQQMPPPEEPL 384 score: Perfect

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A Geneseq 16Dec04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:

## SUMMARIES

Description		_	-	_	Human	Human	Abg31586 Human sph	Ade38365 Human pro	Human	Human	Human	Humar		Adj75441 Marker ge	Marker	Human	Human		9 Human	Mouse	Mouse		80	Marker	Aay56053 Mouse sph
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Score	2017	2017	2013	2013	2013	2013	2013	2013	2008	2005	2005	2004	1997	1996	1996	1996	1959	1920	1749	1636.5	1629.5	1627.5	1627.5	1627.5	1624.5
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## ALIGNMENTS

Sphingosine kinase; antiarthritic; antiasthmatic; antiarteriosclerotic; antiinflammatory; neuroprotective; antibacterial; immunosuppressive; Human sphingosine kinase protein sequence. AAB48007 standard; protein; 384 AA (first entry) WO200070028-A1. Homo sapiens. 19-MAR-2001 AAB48007; human. AAB48007 

23-NOV-2000.

12-MAY-2000; 2000WO-AU000457.

99AU-00000339. 99AU-00001504. 13-MAY-1999; 08-JUL-1999;

(JOHJ ) JOHNSON & JOHNSON RES PTY LTD.

Gamble JR; D'andrea RJ, Xia P, Wattenberg BW, SM, Vadas MA; Pitson

WPI; 2001-016227/02. N-PSDB; AAC84161.

Novel sphingosine kinase protein and nucleic acid molecules for diagnosis, prophylaxis and treatment of rheumatoid arthritis, asthma, atherosclerosis, inflammation, meningitis, multiple sclerosis and septic

Claim 9; Fig 7a; 100pp; English.

This represents a human sphingosine kinase (SK) protein. The human SK protein, encoding nucleic acids and modulators are useful for modulating expression, functional activity or cellular functional activity of sphingosine kinase in a subject and also for treating a mammal by modulating the activity of SK. Diseases treated by regulating SK cellular activity include rheumatoid arthritis, asthma, atherosclerosis, inflammation, meningitis, multiple sclerosis and septic shock

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21-JAN-2003; 2003AU-00900230.
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                                                                    Pitson SM, Xia P,
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                                  Length 384;
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                                  Score 2017; DB 4;
Pred. No. 7.5e-210;
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08-APR-2002;
19-SEP-2002;
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Sequence 384
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The invention relates to modulating sphingosine kinase (SK) functional activity. The method involves contacting the SK with an agent for a time and under conditions to modulate phosphorylation of the SK where inducing or agonizing the phosphorylation of the SK activity and inhibiting or antagonizing the phosphorylation down regulates SK activity. The modulation of the phosphorylation is modulation of proline-directed protein kinase catalyzed phosphorylation. The proline-directed frinase is ERK1, ERK2 or CDK2. The modulation is preferably down-regulation. The methods and agents are useful for treating and/or prophylaxis, of a condition characterized by aberrant, unwanted or inappropriate cellular activity or sphingosine kinase functional activity, e.g. a meoplastic condition or an inflammatory condition such as rheumatoid arthritis, atherosclerosis, asthma, autoimmune disease or inflammatory bowel disease. The present sequence represents a human SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60
                                                                                Wattenberg BW;
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                                                                                Vadas MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2017; DB 7;
100.0%; Pred. No. 7.5e-210;
iive 0; Mismatches 0;
                                                                            Verwey JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 12; 95pp; English.
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                                                                                Moretti PA,
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(MEDV-) MEDVET SCI PTY LTD
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Pred. No. 2e-209;

99.78;

Similarity

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N-PSDB; AAA75676. Кеу 

2000-602121/57

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Human; intracellular phosphorylation regulator; HRIP; stroke; myeloma;
                                                     neurological disorder; Parkinson's disease; demyelinating disease; meningitis; developmental disorder; neuromuscular disorder; cancer; myasthenia gravis; cell proliferative disorder; actinic keratosis; arteriosclerosis; leukaemia; melanoma; bronchitis; autoimmune disorder; inflammatory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus; rheumatoid arthritis; microbial infection; trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Azimzai Y;
                                                                                                                                                                                                                                                                                                                   16. .153
/note= "diacylglycerol kinase catalytic site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "potential glycosylation site"
human regulator of intracellular phosphorylation.
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                                                                                                                                                                                                                                                                                           Location/Qualifiers
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99US-0135049P.
99US-0143188P.
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The present sequence represents a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and anteaponists and attagonists or anteagonist or anteagonist or screening adjaces or condition associated with decreased or increased expression of functional HRIP. Diseases treated or diagnosed include neurological disorders such as stroke, Parkinson's disease, accertization of viral meniagitis and other developmental disorders of the central nervous system, neuromuscular disorders, myasthenia gravis, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer including leukammia, melanoma, myeloma and cancer of the adrenal gland, bladder, bone, bone marrow, liver, lung, muscle, ovary, autoimmune/ inflammatory disorder such as Addison's disease, acquired immunodeficiency diseases, allegies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial Novel human intracellular phosphorylation regulator polypeptides and polymucleotides for diagnosis, prevention and treatment of neurological, cell proliferative and autoimmune/inflammatory disorders. Claim 1; Page 77-78; 96pp; English infection and trauma

Sequence 384 AA;

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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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                                                                                                                                            SEKYRRIGEMRFTLGTFLRALALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
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                                                                               RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL
                                                                                             61 RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL
                                MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
                                              NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE
                                                                                                                                                                              SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
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           Gaps
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           Indels
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Otsuki
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Wakamatsu A, Nagai K,
           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                            AAB94589 standard; protein; 384 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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            383; Conservative
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27-AUG-1999;
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            Matches
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us-10-642-289-2.rag

07-FEB-2001

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complementary strand of a polynucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence 53'-end sequence 53'-end sequence 53'-end sequence 63'-end 64-end 6
          Where a primer set comprises:
          length cDNAs defined in the specification.
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Sequence 384 AA;

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SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGFVDAHLVP 240
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                                                                          1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
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 Score 2013; DB 4; Length 384;
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                Pred. No. 2e-209;
1; Mismatches
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                             Matches 383; Conservative
                Local Similarity
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Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                            Human protein sequence SEQ ID NO:13997
          Ā
          AAB93955 standard; protein; 384
                                           26-JUN-2001 (first entry)
                                                                                              Homo sapiens
                          AAB93955;
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EP1074617-A2

LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPWGRCAAGVWHLFYVRAGVSRAMLL 300

241

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NHYAGYEQVTNEDLLITNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
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                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
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                                                                                                                                Yamamoto J;
                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 13997; 2537pp + Sequence Listing; English.
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                                                                                                                               Saito K,
, Otsuki
                                                                                                                                         Wakamatsu A, Nagai K,
                                                                                                                                Hayashi K,
                                                     27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                     28-JUL-2000; 2000EP-00116126.
                                                                                                                                Nishikawa
                                           99JP-00248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 383; Conservative
                                                                                                         (HELI-) HELIX RES INST
                                                                                                                                          Sugiyama T,
                                                                                                                                                              WPI; 2001-318749/34.
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                                                                                                                                Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention
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                                         29-JUL-1999;
                                                                                                                             Ota T, Is
Ishii S,
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Gaps

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Length 384; 0; Indels

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Score 2013; DB 4, Pred. No. 2e-209; 1; Mismatches (

99.8%;

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| MDPAGGPRGVLPRPCRVLVLLNPRGGRGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE

19 19

1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA

240

SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP

LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW

120 180 180 360 360

MVSGCVEPPSWKPQQMPPPEEPL 384 

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181 SEKYRRIGEMRFTLGTFLRAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
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                             Best Local Similarity 99.7
Matches 383; Conservative
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                                                                                                                                                                                                                                                                                                               Human; sphingosine kinase type 1; skl; chromosome 17q25.2; sphingosine-1-phosphate; S1P; drug screening; therapy; haemostasis; thrombosis; allergic reaction; proliferative disease; cancer; haematopoietic disorder; leukaemia; cardiovascular disease; stroke; atherosclerosis; coronary artery disease; dyslipidaemia; diabetes; autoimmune disease; inflammatory disease; multiple sclerosis; T helper-1 related disease; chronic Obstructive pulmonary disease; esthma; myocardial infarction; neurodegenerative disorder; wound healing; embryogenesis; anticoagulant; cerebroprotective; neuroprotective; antipsoriatic; antiarthritic; cytostatic; cardiant; vulnerary.
 360
                   RIFILAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is human sphingosine kinase type 1 (hskl). The hskl gene is located on chromosome 17q25.2. The skl converts the substrate sphingosine to sphingosine-1-phosphate (SIP). The skl gene and encoded polypeptide are applicable in screening drug candidates particularly inhibitors for preventing or treating disorders such as haemostasis, haematopoisis, allergic reactions, proliferative diseases including cancer, haematopoisters such as Proliferative diseases including cancer, haematopoisters such as Beukaemia, cardiovascular diseases such as stroke, atherosclerosis and coronary artery disease, dyslipidaemia, diabetee including type I and type II diabetes, autoimmune and inflammatory diseases such as multiple sclerosis, Thelper-1 related diseases, chronic obstructive pulmonary disease, asthma, myocardial infarction, neurodegenerative disorders, natural wound healing processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human sphingosine kinase type I gene for screening drug candidates particularly inhibitors used for preventing or treating e.g. atherosclerosis, thrombosis, asthma and diabetes.
RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW
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/label= Conserved region
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                                                                                            MVSGCVEPPPSWKPQQMPPPEEPL 384
                                                                    MVSGCVEPPPSWKPQQMPPPEEPL 384
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07-FEB-2000; 2000US-0180525P
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                                                                                                                                                                                                                                                        (first entry)
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Human; sphingosine kinase 1; SPHK1; blood vessel formation; primate; congestive heart failure; myocardial ischaemia; wound healing; ischaemia-reperfusion injury; peripheral arterial disease; anglogenesis; coronary artery disease; peripheral vascular disease; fracture repair; reconstructive surgery; transplantation; islet transplant; tendon repair; sports injury; ulcer; thromboangitis obliterans; Buerger's disease; periodontal tissue regeneration; radiotherapy-induced oesophagitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing blood vessel formation, or preventing/treating congestive heart failure, ischemia-reperfusion injury, myocardial ischemia and peripheral arterial diseases in animal, by administering sphingosine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                      (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                    Human sphingosine kinase 1 (SPHK1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Su J;
                                                                                                                                                                                                                                                                                                                                            05-OCT-2001; 2001WO-EP011513
                                                                                                                                                                                                                                                                                                                                                                         05-OCT-2000; 2000US-0238230P
                                                        (first entry)
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                                                          05-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liau G,
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Sequence 384 AA;

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formation in an animal. The method of the invention involves administering sphingosine kinase to the animal. The method is useful for inducing blood vessel formation in an animal. The method is useful for inducing blood vessel formation in an animal. The method is useful for congestive heart failure, myocardial ischaemia, ischaemia reperfusion injury and peripheral arterial diseases in an animal, e.g. mammal (such as primate including human). The invention is also useful for treating diseases or disorders selected from coronary artery disease, peripheral vascular disease, wound healing and fracture repair, reconstructive surgery, transplantation such as islet transplants, tendon repair/sports injury, healing of ulcers, thromboangitis obliterans (Buerger's disease), periodontal tissue regeneration and radiotherapy-induced oesophagitis. The present amino acid sequence represents the human sphingosine kinase I (SPHKI) protein as described in the invention
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                                                          present invention relates to a new method of inducing blood vessel
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Pred. No. 2e-209;
1; Mismatches 0;
                  Disclosure; Page 35-36; 45pp; English.
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tumourigenic disorder; angiogenic disorder; aberrant gene expression; aberrant protein activity; cytostatic; antithyroid; antidiabetic; ophthalmological; cancer; breast cancer; clon cancer; lung cancer; prostatic cancer; dispetic retinopathy; protein 49863.
                                                                                                           Human protein 49863 amino acid sequence.
                           ADE38365 standard; protein; 384
                                                                               29-JAN-2004 (first entry)
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                                                     ADE38365;
RESULT 8
ADE38365
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07-AUG-2003

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having a tumourigenic disorder or angiogenic disorder, caused by aberrant gene expression or activity of an isolated protein, by administering a modulator. The modulator may have eytostatic, antithyroid, antitidabetic or ophthalmological activity. The method is useful for treating a subject having a tumourigenic or angiogenic disorder, in particular for treating cancer (for example breast cancer, colon cancer, lung cancer or prostatic cancer) and, for example, Grave's disease and diabetic retinopathy. The present sequence is the amino acid sequence of the novel isolated human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating subject having tumorigenic disorder or angiogenic disorder caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid, by administering a modulator
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hunter JJ, Macbeth KJ, Tsai F, Williamson MW, Rudolph-Owen LA;
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                                                              15-MAR-2002; 2002US-0364517P.
09-ARR-2002; 2002US-0311075F.
10-ARR-2002; 2002US-0371507P.
16-APR-2002; 2002US-0372984P.
19-APR-2002; 2002US-0374194P.
24-MAY-2002; 2002US-038295P.
31-MAY-2002; 2002US-038295P.
                                                                                                                                                            2002US-0385023P.
2002US-0388853P.
2002US-0389395P.
2002US-0391324P.
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22-AUG-2002; 2002US-0405155P.
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25-OCT-2002; 2002US-0421195P.
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               30-JAN-2003; 2003WO-US002588
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Best Local Similarity 99.7
Matches 383; Conservative
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N-PSDB; ADE38364
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang D;
, Zhao QA;
LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
                       RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW 360
                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                               Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ren F, Wa
Zhang J,
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Yang Y,
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Xue AJ,
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                                                                     MVSGCVEPPSWKPQQMPPPEEPL 384
                                                                                   Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  манд z, wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                       AAM40180 standard; protein; 384 AA
                                                                                                                                                                                                                           polypeptide SEQ ID NO 3325.
                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-0048725.
25-APR-2000; 2000US-0052317.
25-JUN-2000; 2000US-00598043.
19-JUL-2000; 2000US-00520312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2000; 2000WO-US034263
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Wang Z, Wehrman T,
                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                             leukaemia.
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Zhou P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVWHLFYVRAGVSRAMLL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sphingosine kinase; SPHK; SPHK1; cytostatic; vasotropic; antidiabetic;
                                                                                                                                                                                                                              1 MDPAGGPRGVLPRPCRVLVLINPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
                                                                                                                                                                                                                                                                                                RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 LEEPUPSHWTVVPDBDFVLVLALLHSHLGSEMFAAPMGRCAAGVWHLFYVRAGVSRAMLL
\text{C.N.S} disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                    1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
                                                                                                                                                            Gaps
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                                                                                                              Length 384;
                                                                                                                                                          1; Indels
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                                                                                                         Score 2008; DB 4;
Pred. No. 7.2e-209;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 MVSGCVEPPSWKPQQMPPPEEPL 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32-MAR-2001; 2001US-00796487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2000; 2000US-0186352P.
                                                                                                              Query Match 99.6%;
Best Local Similarity 99.5%;
Matches 382; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SPIE/) SPIEGEL S.
                                                                      Sequence 384 AA;
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          (SPHK) DNA. Cells
The invention relates to an isolated sphingosine kinase (SPHK) DNA. Cells transformed with SPHK DNA are used to screen for agents that reduce, eliminate or promote SPHK activity. Agents that inhibit activity are useful for decreasing cell proliferation, e.g. for treating cancer, and for treating diseases associated with abnormal migration and motility of cells, e.g. restenosis or diabetic neuropathy. Agents that increase activity are used to reduce cell death. Antibodies raised against SPHK, and primers or oligonucleotides derived from the DNA are useful for diagnosis. The antibodies are also useful as therapeutic inhibitors. The present sequence represents a human sphingosine kinase 1 (hSPHK1)
                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
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                                                                                                                                                                                                                                                                                                                     Length 384;
                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                     Score 2005; DB 5;
Pred. No. 1.5e-208;
                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                     99.4%;
                                                                                                                                                                                                                                                                                                                                                                        Matches 380; Conservative
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                           Sequence 384 AA,
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240 240 300 360 120 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180 180 RFFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFW 360 RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120 9 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL NHYAGYEQVTNEDLLINCTLLLCRRILSPMNLLSLHTASGLRLFSVLSLAMGFIADVDLE SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP LEEPVPSHWTWVPDEDFVLILALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVOGOVHPNYFW SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL MVSGCVEPPSWKPQQMPPPEEPL 384 MVSGCVEPPPSWKPQQMPPPEEPL 384 61 121 241 19 121 181 181 241 301 301 361 361 8 셤 ઠે 유 ઠ 요 ò 셤 ò 셤 Š 셤 ò g

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> Human soft tissue sarcoma-upregulated protein ADQ17905 standard; protein; 384 26-AUG-2004 (first entry) WO2004048938-A2 Homo sapiens 10-JUN-2004. ADQ17905;

- SEQ ID 722

soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

(PROT-) PROTEIN DESIGN LABS INC. 26-NOV-2003; 2003WO-US038193. 26-NOV-2002; 2002US-0429739P.

Zlotnik A; Ginsburg WM, Aziz N,

WPI; 2004-441208/41

Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue

SEQ ID NO 722; 210pp; English Example 2;

The invention relates to a novel method for detecting soft tissue sarcome which comprises obtaining a first soft tissue sample from an individual data and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic scil sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor. 

Sequence 384 AA;

ö 61 RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120 121 NHYAGYEQVTNEDLLTNCTLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180 181 SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300 RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW 360 9 1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETALQKPLCSLPAGSGNALAASL 1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP ö 99.4%; Score 2005; DB 8; Length 384; 99.0%; Pred. No. 1.5e-208; Indels 3; Mismatches 384 MVSGCVEPPSWKPQQMPPPEEPL 384 MVSGCVEPPPSWKPQQMPPPEEPL Matches 380; Conservative Similarity 121 241 181 301 301 361 361 Query Match Local

ABP71054 standard; protein; 384 AA Human sphingosine kinase. 14-APR-2003 ABP71054; 요

TNF; tumour necrosis factor; sphingosine kinase; TRAF; TRAF2; cytostatic; TNF receptor-associated factor; antiinflammatory; antirheumatic; human; antiarthritic.

Homo sapiens

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The invention relates to modulating cytokine-induced or tumour necrosis factor (TNF)-induced cellular activity. The method involves contacting the cell with an agent under conditions sufficient to modulate the interaction of sphingosine kinase with a TNF receptor-associated factor (TRAF), preferably TRAF2, where inducing the association up-regulates cellular activity, and inhibiting the association down-regulates cellular activity. The agent is useful for manufacturing a medicament for treating a mammal with a condition of aberrant, unwanted or inappropriate cytokine condulating or preventing a condition of aberrant, unwanted or inappropriate cytokine-induced or TNF-induced cellular activity, or for creating or preventing a condition of aberrant, unwanted or inappropriate cytokine-induced or TNF-induced cellular activity in a mammal, such as neoplastic condition or inflammation (e.g. rheumatoid arthritis). The present sequence represents a human sphingosine kinase
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                                                                                                                                                                                                                                                                                                                                                                                   Modulating cytokine- or tumor necrosis factor-induced cellular activity, useful for treating or preventing a neoplastic condition, comprises modulating an intracellular sphingosine kinase-dependent signaling
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                                                                                                                                                                                                                                                                                                                   Gamble J, Moretti P, Pitson
                                                                     /note= "specifically claimed peptide"
                                  /note= "Xaa is unknown"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Fig 9; 96pp; English.
                                                                                                                                                                           03-JUN-2002; 2002WO-AU000710.
                                                                                                                                                                                                              07-JUN-2001; 2001AU-00005521
                                                                                                                                                                                                                               13-AUG-2001; 2001AU-00006978.
27-DEC-2001; 2001AU-00009759
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                                                                                                                                                                                                                                                                                                                      Wang L,
                    Misc-difference
                                                                                                          WO200298458-A1
                                                                                                                                         12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mechanism.
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     요
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The present sequence is that of human sphingosine kinase A (SKA), an enzyme that phosphorylates sphingosine to form sphingosine 1-phosphate. The sequence was deduced from that of a polymuclectide (see AAASOSOB) isolated from an Hela cDNA library. The invention provides polymuclectides (see AAASOSOB-10) and polypeptides can be obtained using recombinant DNA methods, and host colls containing expression vectors including SK polymuclectides are used in a claimed method of screening for compounds that inhibit or activate their analogues can be used as bioactive agents to treat inflammation or their analogues can be used as bioactive agents to treat inflammation or disease including viral, bacterial or fungal infections, allergic responses, mechanical injury associated with trauma, hereditary diseases, lymphoma or carcinoma, and other conditions with activate the genes of kidney, lung, heart, lymphoid or tissues of the nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine kinase expression.
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                                                                                                                                                                                                                                                                Sphingosine kinase A; SKA; human; drug screening; infection; antiinflammatory; antiallergic; anticancer; inflammation; allergy; cancer; therapy; diagnosis.
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                361 MVSGCVEPPPSWKPQQMPPPEEPL 384
                                                                                                                        AAY96057 standard; protein; 384 AA
361 MVSGCVEPPSWKPQQMPPPEEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 3; 81pp; English.
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                                                                                                                                                                                                                                Human sphingosine kinase A.
                                                                                                                                                                                                (first entry)
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Best Local Similarity 99.0°
Matches 380; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 WO200052173-A2
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an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial cobstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene, a ribosyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising control encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for resting for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present corrective bronchial asthma or chronic obstructive pulmonary disease. The present

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                                                                                                                                RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW 360
                                                                                                                                            RIFLAMEKGRHMEYECPYLVYVPVVAFRIEPKDGKGVFAVDGELMVRRAVQGQVHPNYFW 360
NHYAGYEQVINEDLLINCILLICRRLLSPMNLLSLHTASGIRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.
                                                                                                                                                                                                                                                                                                                                            bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                       SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
                                                                                     LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL
                                         SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Izuhara K;
                                                                                                                                                                                                                                                                                                                       Marker gene related amino acid sequence SEQ ID NO:693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11; SEQ ID NO 693; 241pp; English.
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                                                                                                                                                                           MVSGCVEPPSWKPQQMPPFEFPL 384
                                                                                                                                                                                       MVSGCVEPPPSWKPQQMPPPEEPL 384
                                                                                                                                                                                                                                                      ADJ75441 standard; protein; 398 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-2002; 2002JP-00229312.
20-MAR-2003; 2003JP-00077212.
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                                                                                                                                                                                                                                                                                                20-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                  gene therapy; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohtani N, Sugita Y,
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                                                                                                                                                                                                                                                                                                                                                               SLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSV 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                                                                                                 47 ISFTLMLTERRNHARELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLC
                                                                                                                                                                                                                                                                                                                                                                              SLPAGSGNALAASLNHYYAGYEQVTNEDILTNCTLILCRRILSPMNLLSLHTASGLRLFSV
                                                                                                                                                                                                                                                                                                                                                                                                                             241 VVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMH
                                                                                                                                                                                                                                                                  1 MDP-------AGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAE
                                                                                                                                                                                                                                                                                                                                                                                                               167 LSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMH
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                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                  Length 398;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marker gene related amino acid sequence SEQ ID NO:639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEAVQQVHPNYFWMVSGCVEPPSWKPQQMPPPEEPL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL 384
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                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; marker.
                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                           Sequence 398 AA;
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nes 383;
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for esting for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3)

06-AUG-2002; 2002JP-00229312. 20-MAR-2003; 2003JP-00077212.

(GENO-) GENOX RES INC.

Izuhara Nagai H, Kubo H, Уатауа М, Sugita Y, Ohtani N,

WPI; 2004-193155/19.

Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.

Example 11; SEQ ID NO 639; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (l) a reagent (l) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (4) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a naminal model for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an animal model for bronchial asthma or chronic obstructive pulmonary disease, comprising to a portion of the marker gene or an animal model for bronchial asthma or chronic obstructive pulmonary disease, comprising to a protein encoded by a marker gene; and (7) a DNA chip for testing for c spronehial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene; and the gene through obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (I) has respiratory conditional asthma or chronic obstructive pulmonary disease. The present cy sequence is used in the exemplification of the present invention.

Sequence 398 AA;

SLPAGSGNALAASINHYAGYEQVTNEDLITNCTLLLCRRLLSPMNLLSIHTASGLRLFSV 166 SLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSV 180 226 ISPTIMITERRNHARELVRSEELGRWDALVVMSGDGIMHEVVNGLMERPDWETAIQKPLC 106 1 MDP-----AGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAE 46 9 167 LSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASP Gaps 0; Indels 14; 99.0%; Score 1996; DB 8; Length 398; 96.2%; Pred. No. 1.5e-207; ive 1; Mismatches 0; Indels 1-Local Similarity 96.2 Les 383; Conservative 47 61 107 121 181 Query Match g ઠે g g Š 셤 ò

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VVVQQQPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAFMGRCAAGVMH 300

VVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMH

227

à 용 287 LFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMV 346

361 SEAVÇĞQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL 398 347 ò

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Sequence 11, Appli
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Sequence 11, Appli
Sequence 12617, A
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                                                                                                June 17, 2005, 03:38:14; Search time 237 Seconds (without alignments) 8319.466 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-12882

US-09-949-016-12882

US-09-949-016-13982

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US-09-902-540-1677

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Sequence 5411, Ap Patent No. 5256770 Sequence 1263, Ap Sequence 1263, Ap Sequence 1350, Ap Sequence 1099, Ap Sequence 56, Appl Sequence 67, Appl Sequence 1078, Ap Sequence 1070, Ap Sequence 9668, Ap Sequence 1096, App Sequence 1096, App Sequence 1, Appli		Length 1205; indels 0; Gaps 0; cacceccccccccccccc 60	60		CTGAGGCTGAAATCTCCTTCA 180 	rggrgcggrcggaggrgg 240
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GENERAL INFORMATION:

GENERAL INFORMATION:

JETTLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR PELLING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1155

LENGTH: 1783
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iive 0; Mismatches 19;
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Patent No. 6812339
GENERAL INFORMATION:
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Best Local Similarity 98.4
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ORGANISM: Human
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BARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,910
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-07-130
NUMBER OF SEQ ID NOS: 1227

EARLIER PILING DATE: 1998-07-130

SEQ ID NO 90

LENGTHALE PILING DATE: 1998-07-30
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                                                                                  R APPLICATION NUMBER: 60/048,893
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,900
R PILING DATE: 1997-06-06
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R FILING DATE: 1997-06-06
R PILING DATE: 1997-06-06
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R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,915
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                          APPLICATION NUMBER: 60/048,899
FILING DATE: 1997-06-06
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
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NAME/KEY: SITE
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GENERAL INFORMATION:
JETLE REPERBURE:
PROJOTPI
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: EVT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,895
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,954
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; Sequence 90, Application US/09205258
; Patent No. 6525174
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RESULT 4
US-09-970-516-1
US-09-970-516-1
Sequence 1, Application US/09970516
Patent No. 6610534
GENERAL INFORMATION:
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION UNMBER: US/09/970,516
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCACTGCACGCTA 420
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                                                             AAGGATGGGAAAGGTATGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAG
                                                                                       1067 AAGGATGGGAAAAGGTGTGTTTGCAGTGGGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAG
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Pred. No. 5.5e-268;
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larity 99.6%;
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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                     n equals a,t,g,
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  ; LOCATION: (1527)
; OTHER INFORMATION:
US-09-205-258-90
LOCATION: (1527)
                                                                                Query Match
Best Local Simi
Matches 1164;
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                               Length 1764;
                                                      46; Indels
                               DB 4;
                              Score 1081.4; DB 4;
Pred. No. 4.6e-252;
0; Mismatches 46;
                               89.78;
                                 Query Match 89.7
Best Local Similarity 95.8
Matches 1133; Conservative
ORGANISM: Human
    ; OKGANISM: HUMAI
US-09-949-016-3940
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; Sequence 3940, Application US/09949016
; Batent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLOU3307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PLILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3940
LENGTH: 1764
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Sequence 15682, Application US/09949016
; Sequence 15682, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANTY VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE REPRENCE: CLOOD.307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR PILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15682
; LENGTH: 7198
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 12897

SEQ ID NO 12897
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Patent No. 6610534
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
TITLE OF INVENTION: US/09/970,516
CURRENT APPLICATION NUMBER: US/09/970,516
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                40.8%; Score 491.4; DB 4; 99.4%; Pred. No. 1.9e-109; ive 1; Mismatches 2;
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1138 GAAGAACCATAA 1149
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Best Local Similarity 99.4
Matches 492; Conservative
                                              US-09-949-016-40620
                                                                                                                                                                                                                                                                                               ORGANISM: Human
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                                                                                                                                                                                                                                                          SEQ ID NO 40620
LENGTH: 601
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US-09-949-016-139382 ; Sequence 139382, Application US/09949016 ; Patent No. 6812339

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JAPULICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILE OF INTERNION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 139382

LENGTH: 601
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Patent No. 6610534

GENERAL INFORMATION: GENERAL SAG

TITLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: polynucleotides encoding sphingosine kinases

FILE REFERENCE: 4-31617

CURRENT APPLICATION NUMBER: US/09/970,516

CURRENT FILING DATE: 2001-10-04
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40.8%; Score 491.4; DB 4;
Best Local Similarity 99.4%; Pred. No. 1.9e-109;
Matches 492; Conservative 1; Mismatches 2;
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ORGANISM: Human
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Patent No. 6800470

GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning, TITLE OF INVENTION: Expression and Methods of Use Thereof FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2001-03-26
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Pred. No. 7.8e-53;
0; Mismatches 230; Indels
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Matches 396; Conservative
                            SOFTWARE: Patentin version SEQ ID NO 3
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(1857)
OTHER INFORMATION:
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TITLE: Molecular cloning and functional characterization;
TITLE: novel mammalian sphingosine kinase type 2 isoform;
JOURNAL: J. Biol. Chem.
JOURNAL: 275
ISSUE: 26
PAGES: 19513-19520
PATE: 2000-06-30
DATE: 2000-06-30
DATES ACCESSION NUMBER: AF245447
DATABASE ACCESSION NUMBER: 2000-06-27
US-09-817-676A-13
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PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (7)..(1860)
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 GGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGAGACGGGCTGATGCACGA 289
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                                                    APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 2698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 GGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCCATCCAGAAGCCCCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (387)..(2237)
PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization of
TITLE: novel mammalian sphingosine kinase type 2 isoform
VOLUME: J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.3%; Score 245.2; DB 4; Best Local Similarity 62.0%; Pred. No. 1.1e-49; Matches 388; Conservative 0; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATE: 2000-06-30
DATABASE ACCESSION NUMBER: AF245448
DATABASE ENTRY DATE: 2000-06-27
Sequence 11, Application US/09817676A Patent No. 6800470
                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES: 19513-19520
                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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Best Local S
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Sequence 17081, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
Patent No. 6812339

GENERAL INFORMATION:
PLICART: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 10550
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128 GCTCTTCCGGAGTCACGTGCAGCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGAT 187
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US-09-270-767-12677

Sequence 12677, Application US/09270767

Sequence 12677, Application US/09270767

Fatent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 12677

LENGTH: 1012
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                                                                                                                                                                                                                                                                    TYPE: DNA; CRGANISM: Drosophila melanogaster
US-09-270-767-12677
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Best Local Similarity 55.81
Matches 150; Conservative
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Search completed: June 17, 2005, 06:47:30 Job time : 240 secs

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June 17, 2005, 05:29:48; Search time 1910 Seconds (without alignments) 3916.279 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_DEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_DEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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1205
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 1, Appli	Sequence 225, App	Sequence 25, Appl	Sequence 721, App	Sequence 90, Appl	Sequence 90, Appl	fund 00 annumen
SUMMARIES		, QI	19 US-10-642-289-1	US-10-335-053-225	US-10-354-358-25	US-10-723-860-721	US-09-933-767-90	US-10-004-860-90	10.00.00.00
		DB	19	20	16	20	10		,
		Query Match Length DB ID	!				1533		
	ф	Query	100.0	97.0	6.96	96.5	95.4	95.4	
		Score	1205	1168.6	1168.2	1162.6	1149.4	1149.4	, , , ,
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Sequence 1, Appli Sequence 22, Appli Sequence 22, Appl Sequence 22, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1180, Ap Sequence 1180, Ap	533 3, A 5, A 5, A 5, A 3, A 13, A 77,	- 0	Sequence 659, App Sequence 658, App Sequence 658, App Sequence 69, Appl Sequence 69, Appl Sequence 1756, App Sequence 2781, Appl Sequence 23, Appl Sequence 23, Appl
US-09-970-516-1 US-10-619-344-1 US-10-348-052-22 US-10-622-011-22 US-10-622-011-22 US-10-876-281-1 US-10-676-281-1 US-10-715-117-1	D D DD D	US-10-830-677-13 US-10-737-450-139 US-09-817-676-11 US-10-425-115-155 US-09-796-692-2905 US-10-057-4758-29 US-10-057-4758-29 US-10-057-4758-29	US-10-764-324-2905 US-09-777-564-658 US-10-015-219-658 US-10-296-115-69 US-10-283-975A-584 US-09-954-456-1756 US-10-843-644A-4783 US-10-168-589-23
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## ALIGNMENTS

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WS-10-64-289-1

WS-10-64-289-1

Sequence 1, Application US/10642289

Publication No. US20040132053A1

GENERAL INFORMATION:

APPLICANT: Brian, WATTENBERG W

APPLICANT: Brian, WATTENBERG W

APPLICANT: Richard, D'ANDREA J

APPLICANT: Mathew, VADAS A

TITILE OF INVENTION: SPHINGOSINE KINASE ENZYME

FILE REFERENCE: PITSON-1

CURRENT APPLICATION NUMBER: US/10/642,289

CURRENT FILING DATE: 2001-11-13

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 56

SOSTWARE: PATENTING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 56

SOSTWARE: PATENTING DATE: 1998-07-08

TYPE: DNA

CURRENT PATENTING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 56

SOSTWARE: PATENTING DATE: 1998-07-08

TYPE: DNA

CENTREL DNA

CENTREL DNA

SEQ ID NO 1

SEATURE: TYPE: DNA

TYPE: DNA

SEATURE: TYPE: DNA
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Sequence 225. Application US/10335053
Publication No. US20040241653A1
GENERAL INFORMATION:
APPLICANT: OLARK Blotech, Inc.
TITLE OF INVENTION: Methods for identifying marker genes for cancer;
TITLE OF INVENTION: Wethods for 105/1051
CURRENT APPLICATION NUMBER: US/10/335,053
CURRENT PILING DATE: 2003-03-27
PRIOR PILING DATE: 2003-03-27
PRIOR PILING DATE: 2001-12-31
PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn version 3.2
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Pred. No. 0;
0; Mismatches
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99.2%;
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US-10-335-053-225
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LENGTH: 2137
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                                                           100.0%; Score 1205;
100.0%; Pred. No. 0;
ative 0; Mismatches
                                                                        Best Local Similarity 100.
Matches 1205; Conservative
; NAME/KEY: CDS
; LOCATION: (33)..(1184)
; OTHER INFORMATION:
US-10-642-289-1
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OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
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         THILE REFERENCE: MPIO2-020PLRNOWNIM
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILIDRO DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR PILING DATE: 2002-01-31
PRIOR PILING DATE: 2002-01-35
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 2002-04-10
PRIOR PILING DATE: 2002-04-10
PRIOR PILING DATE: 2002-04-10
PRIOR PILING DATE: 2002-04-16
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-17
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; LOCATION: (359)...(1513)
US-10-354-358-25
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ORGANISM: Homo sapiens
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; Sequence 721, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: WHERE: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; REIOR APPLICATION NUMBER: 60/429,739
; REIOR PILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
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CRGANISM: HOMO
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US-10-723-860-721
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OTHER INFORMATION: n equals a, t, g, or c
PRIOR APPLICATION NUMBER: 60/048,916
PRIOR PILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/095,923
PRIOR APPLICATION NUMBER: 60/095,923
PRIOR APPLICATION NUMBER: 60/095,923
PRIOR APPLICATION NUMBER: 60/095,923
PRIOR PILING DATE: 1998-05-18
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LOCATION: (123)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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                            1391 GCCAGGTGCACCCCAAACTACTTCTGGATGGTCAGTGGTTGCGTGGAGCCCCCGCCCAGCT 1450
           GCCAGGTGCACCCAAACTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCT 1146
                                                                                  1147 GGAAGCCCCAGCAGCACCGCCAGAAGAGCCCTTATGATCTAGAGTCGAC 1199
                                                                                                     PILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/048,972
                                                                                                                                                                                                               Sequence 90, Application US/09933767
Publication No. US20030181692A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                Sequence 90, Application US/10004860
; Publication No. US20030065160A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Pal; NUMBER OF SEQ ID NOS: 1227
; SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: SITE
LOCATION: (1552)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (1527)
OTHER INFORMATION: n equals a,t,g, or c
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Matches 1164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FBATURE:
NAME/KEY: SITE
COCATION: (12)
OTHER INFORMATION: n equ
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LOCATION: (123)
OTHER INFORMATION: n equ
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US-10-004-860-90
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                                                                                                             13; Indels
                                                                             Score 1149.4; DB 10;
Pred. No. 2.2e-312;
6; Mismatches 13; I
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; NAME/KEY: SITE
; LOCATION: (1527)
; OTHER INFORMATION: n equals a,t,g,
US-09-933-767-90
                                                                             Query Match
Best Local Similarity 98.3%;
Matches 1164; Conservative
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US-10-023-282-90
Sequence 90, Application US/10023282
Publication No. US20030092893A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/10/023,282

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ER PILING DATE: 1998-12-04

ER PILING DATE: 1998-12-04

ER APPLICATION NUMBER: PCT/US98/11422

ER PILING DATE: 1998-06-04

ER APPLICATION NUMBER: 60/048,885

ER PILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/049,375

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,881

ER PILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,880
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EN APPLICATION NUMBER: 60/048,916

EN FILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,373

EN PILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,875

EN FILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,917

EN FILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,917

EN PILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,949

EN FILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,949

EN FILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,897

EN FILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,897

EN PILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,897

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EN APPLICATION NUMBER: 60/048,897

EN FILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,995

EN PILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,962

EN PILING DATE: 1997-06-06

EN APPLICATION NUMBER: 60/048,963
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R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048, 899
R APPLICATION NUMBER: 60/048, 893
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048, 903
R FILING DATE: 1997-06-06
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R FILING DATE: 1997-06-06
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R APPLICATION NUMBER: 60/048,896
R FILING DATE: 1997-06-06
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R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,876
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,972
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APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,895
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,971
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APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
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Sequence 1, Application US/09970516

Parent No. US20020099029A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REPERENCE: 4-31617

CURRENT APPLICATION NUMBER: US/09/970,516

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.1

SEQ ID NO 1
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ORGANISM: Homo sapiens
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; OTHER INFORMATION:
US-09-970-516-1
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NAME/KEY: CDS
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US-09-970-516-1
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EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER PRING DATE: 1997-06-06
EARLIER PRING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PLING DATE: 1997-12-18
EARLIER PLING DATE: 1998-07-15
EARLIER PRING DATE: 1998-07-15
EARLIER PRING DATE: 1998-07-15
EARLIER PRING DATE: 1998-07-15
EARLIER PLING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SEQ ID NO 90
SEQ ID NO 90
LENGTH: 1533
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NAME/KEY: SITE
LOCATION: (12)
OTHER INFORMATION: n equals a,t,g, o:
FEATURE:
NAME/KEY: SITE
LOCATION: (123)
OTHER INFORMATION: n equals a,t,g, o:
FEATURE:
NAME/KEY: SITE
LOCATION: (152)
OTHER INFORMATION: n equals a,t,g, o:
OTHER INFORMATION: n equals a,t,g, o:
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NAME/KEY: SITE
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CTHER INFORMATION: n equals a,t,9,
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Matches 1164; Conservative
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ORGANISM: Homo sapiens
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RESULT 10-619-344-1

Sequence 1, Application US/10619344

Sequence 1, Application US/10619344

Sequence 1, Application No. US20040086487A1

SEGUENCE NO. US20040086487A1

GENERAL INFORMATION:

TITLE OF INVERTION: Induction of blood vessel formation through administration of TITLE OF INVERTION: polynucleotides encoding sphingosine kinases

TITLE OF INVERTION WINDER: US/09/970,344

CURRENT APPLICATION NUMBER: US/09/970,516

PRIOR FILING DATE: 2003-07-14

PRIOR FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 6

SOSTWARE: Patentin version 3.1

SEQ ID NO
1081 AIGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGTGCCACCGCCA 1140
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Pred. No. 1e-311;
0; Mismatches 5;
                                                                   1155
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Best Local Similarity 99.6%;
Matches 1150; Conservative 0
                                                          1141 GAAGAGCCCTTATGA
                                        1173 GAAGAGCCCTTATGA
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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OTHER INFORMATION:
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Sequence 1, Application US/09784810A

Sequence 1, Application US/09784810A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,360
PRIOR APPLICATION NUMBER: 60/182,360
PRIOR PILING DATE: 2000-02-14
PRIOR PILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTION NUMBER: 60/191,261
PRIOR FILING DATE: 2000-03-22
SOFTWARE: PATENTION NUMBER: 2000-03-22
SEQ ID NO 1 ...
LENGTH: 1600
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661 AAGACACCTGCCTCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCA
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                                             CGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTA
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                                                                                             CTGGCACTGCTGCACTCGCACCTGGGCAGTGATGTTTGCTGCACCCATGGGGCCGCTGT
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94.7%; Score 1141.4; DB 9; Length 1600;
Best Local Similarity 97.8%; Pred. No. 3.9e-310;
Matches 1157; Conservative 0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g, other or unknown
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US-09-784-810A-1
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94.8%; Score 1142.4; DB 19; Length 1152;
Best Local Similarity 99.5%; Pred. No. 2e-310;
Matches 1146; Conservative 0; Mismatches 6; Indels 0; (
                                                                                             Sequence 22, Application US/10622011
Publication No. US20040126834A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: OCPPOSITIONS AND METHODS FOR THE MODULATION
TITLE OF INVENTION: OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
FILE REFERENCE: 200116.405C1
CURRENT PRILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
         TYPE: DNA
ORGANISM: Homo sapiens
                                                                         RESULT 11
US-10-622-011-22
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| SABRAMAL INFOGRATION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING | TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING | TITLE OF INVENTION: SAME | SAME | SAME | SAME | SAME | CURRENT APPLICATION NUMBER: US/10/876,281 | CURRENT FILING DATE: 2004-06-24 | PRIOR PAPLICATION NUMBER: US/9/784,810 | PRIOR PAPLICATION NUMBER: 60/182,360 | PRIOR FILING DATE: 2000-02-14 | PRIOR PILING DATE: 2000-02-14 | PRIOR PILING DATE: 2000-02-14 | PRIOR PILING DATE: 2000-03-22 | NUMBER OF SEQ ID NOS: 29 | SEQ ID NOS: 29 | SEQ ID NO 1 | PRIOR PAPLICATION NUMBER: PATENTION NUMBER: PATENTION DATE: 2000-03-22 | NUMBER OF SEQ ID NOS: 29 | SEQ ID NO 1
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                                   ; Sequence 1, Application US/10876281; Publication No. US20050123942A1; GENERAL INFORMATION:
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Best Local Similarity 97.8%;
Matches 1157; Conservative
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US-10-264-237-1180/c

SQUENCE 1180, Application US/10264237

SUBJUCTE 1180. US20040009491A1

GENERAL INFORMATION:

APPLICANT: BITES et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA131P1

CURRENT FAPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR APPLICATION NUMBER: US 60/205,515

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PALENTIN VEY: 3.1

SEQ ID NO 1180

LENGTH: 1562
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NAME/KEY: misc feature
LOCATION: (12)...(12)
COTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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Length 1562;

DB 17;

Score 1140.4;

94.68;

Query Match

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                                                   375 GCGGTTGCGTGCAGCCCCCCCCCCGCCAGCTGGAAGCCCCAGCAGATGCCACCGCAGAAGAGC
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                                                                                                                                                                                                                                                              APPLICANT: L. JING
APPLICANT: EDWERS, SCOTT
APPLICANT: SIN, WIN CHEY
APPLICANT: SIN, WIN CHEY
TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
FILE REPERENCE: 38002-006.
FILE REPERENCE: 38002-003.
CURRENT APPLICATION NUMBER: 60/427,202
PRIOR FILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-11-19
PRIOR FILING DATE: 2002-12-19
                                                                                                                                                                                                                  Sequence 1, Application US/10715117
Publication No. US20040171037A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 1
                                                                                                  1180 CCTTATGATC 1189
                                                                                                                                  CCTTATGACC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-715-117-1
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US-10-715-117-1
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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sw model - protein search, using OM protein

June 15, 2005, 11:44:06; Search time 174 Seconds (without alignments) 1130.106 Million cell updates/sec Run on:

US-10-642-289-2 2017

1 MDPAGGPRGVLPRPCRVLVL......CVEPPPSWKPQQMPPPEEPL 384 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched: 1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q74ZE3	QBN2M3	Q6BW14	Q6CJ88	084501	Q7XXN57	Q9LRB0	07ZW00	CEK1 HUMAN	Q94H <u>Y</u> 9	Q7XCS9	O6GLV1	<u>о</u> 9 FHL3	CEK1_MOUSE
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330	315.5	297	294.5	288.5	273	271	268.5	266.5	265	265	252	250	248.5
32	33	34	35	36	37	38	6	40	41	42	43	44	45

## ALIGNMENTS

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C TISSUE-Mammary gland, and Ovary;

K TISSUE-Ammary gland, and Ovary;

Y DubMed=14702039; DOI=10.1038 M791286;

PubMed=14702039; DOI=10.1038 M791286;

PubMed=14702039; DOI=10.1038 M791286;

A Wakamateu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishi S.,

A Wamanoto J.-I., Sahto K., Yasuda T., Isono Y., Nakamura Y.,

A Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagateuma M.,

Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

Shiratori A., Sudo H., Hosoiri T., Yaku Y., Kodaira H., Kondo H.,

Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,

A Wamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

R Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,

Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
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MEDLINE-20323213; PubMed=10863092; DOI=10.1016/S0378-1119(00)00205-5;
Melendez A.J., Carlos-Dias E., Gosink M., Allen J.M., Takacs L.;
Human sphingosine kinase: molecular cloning, functional
characterization and tissue distribution.";
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MEDLINE-20263733; PubMed=10802064; DOI=10.1016/S0014-5793(00)01510-6;
Nava V.E., Laccana' E., Poulton S., Liu H., Sugiura M., Kono K.,
Milatien S., Kohama T., Spiegel S.,
"Functional characterization of human sphingosine kinase-1.";
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MEDLINE=20407120; PubMed=10947957; DOI=10.1042/0264-6021:3500429;
Pitson S.M., D'Andrea R.J., Vandeleur L., Moretti P.A.B., Xia P.,
Gamble J.R., Vadas M.A., Wattenberg B.W.,
"Human sphingosine kinase: purification, molecular cloning and
characterization of the native and recombinant enzymes.";
Biochem. J. 350:429-441(2000).
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                Q9NYA1; Q9HD92; Q9NY70; Q9NYL3; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) Sphingosine kinase 1 (EC 2.7.1.-) (SK 1) (SPK 1). Name-SPHK1; Synonyme-SPHK, SPK;
                                                                          384 AA
                                                                          PRT;
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                                                                      STANDARD;
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                                                                               SPH1 HUMAN
RESULT 1
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Nomaro J. Kameno J. Kanenio K., Takanelli-Pill A., Hate H., Tanase T-O.,
Nomaro J., Kanello K., Tordiya S., Komai F., Hara R., Takeuthi K., Arica M.,
Noohikawa V., Matsunino K., Yunki H., Obhima A., Sasaki N., Actuaka S.,
Noohikawa K., Sanoh A., Mizoguthi K., Coho, W., Masahima Y., Sano S.,
Noohikawa S., Sanoh A., Mizoguthi H., Coho Y., Bhimizu P., Machella H.,
Noohikawa K., Sanoh A., Mizoguthi H., Coho Y., Shimizu P., Wakbel H.,
Noohikawa K., Sanoh A., Mizoguthi H., Coho Y., Shimizu P., Wakbel H.,
Noohikawa K., Sanoh A., Mizoguthi H., Coho Y., Chinara P., Wakbel H.,
Noohikawa K., Makajia W., Tahilio H., Tanigami N., Phijiara P.,
Noohikawa K., Phiji Y., Cozaki K., Ingaki H., Ikema Y., Okanoto S.,
Noohikawa K., Nakajia W., Tahilio H., Tanigami N., Phijiara P.,
Noohikawa K., Nakajia Y., Mizuno T., Worlinga M., Sanaki M.,
Noohikawa K., Nakajia Y., Mizuno T., Worlinga M., Sanaki M.,
Noohikawa W., Makajia Y., Mizuno T., Worlinga M., Sanaki M.,
Noohikawa W., Nakajia Y., Mizuno T., Worlinga M., Sanaki M.,
Noohikawa W., Nakajia Y., Mizuno T., Worlinga M., Sanaki M.,
Noohika K., Kawaba M., Makajia Y., Mizuno T., Worlinga M., Sanaki M.,
Noohika K., Wakajia Y., Mizuno T., Worlinga M., Sanaki M.,
Noohika K., Wakajia Y., Mizuno T., Worlinga M., Sanaki M.,
Noohika K., Wakajia Y., Mizuno T., Worlinga M., Sanaki M.,
Noohika K., Wakajia Y., Mizuno T., Wolata O., Isogai T., Signati M.,
Noohika K., Wakajia W., Maka M., Makaba M., Makaba M., Maka M
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
                       V -> M (in Ref. 2).
V -> I (in Ref. 2).
V -> F (in Ref. 2).
V -> G (in Ref. 4).
V -> M (in Ref. 3).
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383; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPWNLLSLHTASGLRLFSVLSLAWGFIADVDLE 266
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Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC03053; AAH140553.1; -.
RED; BC030543; AAH14439.1; -.
R GO; GO:0005829; C:cytce01; ISS.
GO; GO:0005829; C:cytce01; ISS.
R GO; GO:0000287; F:D-erythro-sphingosine kinase activity; ISS GO; GO:0017050; F:D-erythro-sphingosine kinase activity; ISS GO; GO:000742; P:D-erythro-sphingosine kinase activity; ISS GO; GO:000742; P:D-erythro-sphingosine kinase activity; ISS GO; GO:000624; P:D-erythro-sphingosine kinase activity; ISS GO; GO:000624; P:D-erythro-sphingosine kinase activity; ISS.
R GO; GO:000624; P:D-erythro-sphingosine kinase activity; ISS.
R GO; GO:000624; P:D-erythro-sphingosine kinase activity; ISS.
R InterPro; IPR001395; Aldo/ket_red.
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 470;
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                                                                                                     Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                       470 AA; 51084 MW; 5172E93A38C7CC17 CRC64;
                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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ProDom; PD005043; DAGKc; 1.
SMART; SM00046; DAGKc; 1.
                                      mouse cDNA sequences.
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SEQUENCE FROM N.A.
                                                                            SEQUENCE FROM N.A.
                                                                                                                                                       TISSUE=Skin;
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Straubberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Haich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleron M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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R GO; GO:0005624; C:cytosol; ISS.
R GO; GO:00017050; F:D-erythno-sphingosine kinase activity; ISS.
R GO; GO:00017050; F:D-erythno-sphingosine kinase activity; ISS.
R GO; GO:0007242; P:intracellular signaling cascade; ISS.
R GO; GO:0007242; P:phingoid catabolism; ISS.
R GO; GO:0046521; P:sphingoid catabolism; ISS.
R InterPro; IPR001206; DAGKC.
R InterPro; IPR001206; DAGKC.
R Priodom; PP005043; DAGKC; I.
R Probom; PP00645; DAGKC; I.
R PROSTITE; PS000665; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
R PROSTITE; PS000663; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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Matches 382, Conservative
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                                                                             NCBI_TaxID=9606;
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Last sequence update) Last annotation update)

01-DEC-2001 (TEMBLE1: 19, 01-DEC-2001 (TEMBLE1: 19, 01-MAR-2004 (TEMBLE1: 26, SPHKI protein:

Created) PRT;

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PRELIMINARY;

**Q96HV8** 

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NHYAGYEQYTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                 47 ISFTLMLTERRNHARELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00063; ALDÓKETO REDUCTASE 3; UNKNOWN 1.
329 AA; 36393 MW; 7F430ABD0CASFDC7_CRC64;
                                                                                                                                                                                                                                                                                                 361 SEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPFEEPL 398
                                                                                                                                                                                                                                                                                  SEAVQGQVHPNYFWMVSGCVEPPSWKPQQMPPPEEPL 384
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ProDom; PD005043; DAGKc; 1.
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                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9541;
                                                                                                                       167
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                                                                                                                                                                                                                                                                                                                                                                                           Q9N0A5;
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Q9N0A5
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                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altasnar F.D., Collins F.S., Wagner L., Schaefer C.R., Bhat N.K.,
Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altachul S.F., Zeeberg B., Bonaldo M.F., Schaefer C.F., Bhat N.K.,
A Brichento D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Andrinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Annes S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDP------AGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAE
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                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.0%; Score 1996; DB 2; Length 398; 96.2%; Pred. No. 2.1e-161; ive 1; Mismatches 0; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 AA; 43944 MW; 7F2C9B26C030E560 CRC64;
                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                     398 AA
                                                        361 MVSGCVEPPPSWKPQQMPPPEEPL 384
                                          MVSGCVEPPPSWKPQQMPPPEEPL 384
                                                                                                                                                             Created)
                                                                                                                                    PRT;
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                           (TrEMBLrel. 19, (TrEMBLrel. 19, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00781; DAGK cat; 1.
ProDom; PD005043; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse cDNA sequences.
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Matches 383; Conservative
                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                   Sphingosine kinase 1.
                                                                                                                                                                                                                              Homo sapiens (Human).
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TISSUE=Kidney;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                      01-MAR-2004
                                                                                                                                                                         01-DEC-2001
                                                                                                                                                                                                                Name=SPHK1;
                301
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                                                                                                                                                                  121 SLPAGSGNALAASINHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSV 180
                                                                                                                                                                                                                                                                                          301 LFYVRAGVSRAMLLKLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 LFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMV 346
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Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

Suzuki Y., Supano S., Hashimoto K.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB046025; BAB01607.1; -.

GO; GO:0005829; C:cytosaol; ISS.

GO; GO:0005829; C:cytosaol; ISS.

GO; GO:0005824; C:membrane fraction; ISS.

GO; GO:000787; F:magnesium ion binding; ISS.

GO; GO:000787; P:sphingoid catabolism; ISS.

HITEPPO; IPR001305; Aldo/ket_red.

InterPro; IPR001206; DAGKC.
                                                                                                                                                                                                                                         LSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASP
                                                                                                                                                                                                                                                                                                                                                                                     VVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDPAGGPRGVLPRSCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unnamed protein product.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Best Local Similarity
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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                 Matches
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Q91ZN3
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Randrarwer/wi illower in the control of the cont
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                                                                                                                    NHYAGYEQVTNEDLLTNCTRLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                  SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
                                                    LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL
                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MGI:1316649; Sphkl.
GO:0005829; C:cytosol; ISS.
GO:0005624; C:membrane fraction; ISS.
GO:0017050; F:D-erythro-sphingosine kinase activity; ISS.
GO:0000287; F:magnesium ion binding; ISS.
GO:0007242; P:intracellular signaling cascade; ISS.
GO:0046521; P:sphingoid catabolism; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037710; AAH37710.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B791FAA58FCE3D29 CRC64;
                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                          382 AA
                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                       RLFLAMEKGRHMEYECPYLVYV 322
                                                                                                                                                                                          382 AA; 42443 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                          23,
23,
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Pfam; PF00781; DAGK_cat; 1.
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                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                           Sphingosine kinase 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                           01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004
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Length 382;

DB 2;

Score 1636.5;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 LEEPVPSHWTVVPEQDFVLVLVLLHTHLSSELFAAPMGRCEAGVWHLFYVRAGVSRAALL
                                                                                                                                                    NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
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                                                                                                        MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
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Sciurognathi; Muridae; Murinae; Mus
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Thompson D., Pyne D., Pyne S.;
Thompson D., Pyne D
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                                    ä
                            39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA; 42344 MW; 2F2C1F10D59EB129 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
Pred. No. 8.4e-131;
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                                34; Mismatches
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Mammalia; Butheria; Rodentia;
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80.78;
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                                    309; Conservative
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                                                                                                                                                         312 QKGKHMELDCPYLVHVPVVAFRLEPRSQRGVFSVDGELMVCGAVQGQVHPNYLMMVCGSR 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 EELGHWDALAVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGGSGNALAASVNHYAGY 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 LGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVWHLFYVRAGVSRAMLLRLFLAM 306
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                                                     252 SHWIYVYPEQDFVLVLVILHTHLSSELFAAPMGRCEAGVWHLFYVRAGVSRAALLRLFLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 PRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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GO; GO:0004143; Fidacylglycerol kinase activity; I
GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKc.
InterPro; IPR001206; DAGKc.
ProDom: PD005043; DAGKc; 1.
SMART; SM00046; DAGKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                504
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J. Biol. Chem. 273:23722-23728(1998).
EMBL; AF068748; AACG1697.1; -.
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                                                                                                                                                                                                                                          367 EPPPSWKPQQMPPPEEP 383
                                                                                                                                                                                                                                                                                             372 DAPSGRDSRRGPPFEFF 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, L. 01-WAR-2004 (TrEMBLrel. 26, L. Sphingosine Kinase (Fragment) Name-Sphkl; Synonyms-SPHKla; Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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01-NOV-1998 (TrEMBLrel.
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SEQUENCE
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                                                                                   SHWTVVPEQDFVLVLVLLHTHLSSELFAAPWGRCEAGVWHLFYVRAGVSRAALLRLFLAM 304
                                                                                                                                                                                                                                                                                                                                                                              EKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFWMVSGCV 366
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EELGHWDALAVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGGSGNALAASVNHYAGY 125
                                                     EQVINEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRR 186
                                                                                                                                                            LGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVP 246
                                                                                                                                                                                                                                                                      SHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAM 306
                                                                                                                                                                                                                                                                                                                                                                                                          72
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J. Biol. Chem. 273:23722-23728(1998).
EMBL; AF068749; AAC61698.1; -.
MGD; MGI:1316649; Sphkl.
GO; GO:0007205; P:protein kinase activity; IEA.
GO; GO:0007205; P:protein kinase C activation; IEA.
Interpro, IPR001206; DAGKC.
Pfam; PF00781; DAGK cat; 1.
Probom; PD005043; DĀGKC; 1.
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Sciurognathi; Muridae; Murinae; Mus.
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; Pred. No. 5e-130;
33; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 388 AA; 43254 MW; 01EB032322542CAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPPSWKPQQMPPPEEP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAPSGRDSRRGPPPEEP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sphingosine kinase.
Name=Sphkl; Synonyms=SPHKlb;
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 307; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00046; DAGKC; 1
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01-MAR-2004
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99
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241 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVWHLFYVRAGVSRAMLL 300
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RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW 360
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                                                                                                                                                                                                                                                                                                                        ©91V26;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Sphingosine kinase 11 (Sphingosine kinase la) (Sphingosine kinase 1c)
(Sphingosine kinase 1d) (Sphingosine kinase la).
Name-sphklf; Synonyms=sphkla, sphklc, sphkld, sphkle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shiota K.;
FigG island of rat sphingosine kinase-1 gene: tissue-dependent DNA
methylation status and multiple alternative first exons.";
Genomics 78:117-125(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li AB049574; BAB62323.1; -. 6000005829; C:cytosol; IS. GO:0005624; C:membrane fraction; ISS. GO:0017050; F:D-erythro-sphingosine kinase activity; ISS. GO:0007051; F:magnesium ion binding; ISS. GO:0007242; P:intracellular signaling cascade; ISS. GO:0007242; P:intracellular signaling cascade; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Imamura I., Obgane J., Ito S., Ogawa T., Hattori N., Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 AA; 42418 MW; CAAD5817BF4B9507 CRC64;
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                                                                                                                                                                                                                                                                                                    383
                                                                                                                                                                            360 MVSGSSDSPSGRDSQRRPPPEEPI 383
                                                                                                                                                    361 MVSGCVEPPSWKPQQMPPEEPL 384
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB049575; BAB62124.1; --
EMBL, AB049571; BAB62320.1; --
EMBL, AB049572; BAB6232.1; --
EMBL, AB049573; BAB6232.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00781; DAGK cat; 1.
ProDom; PD005043; DAGKc; 1.
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Matches 299; Conservative
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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EMBL;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC081738; AAH81738.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                383
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                                                             and mouse cDNA sequences.
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25-OCT-2004
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RE SEQUENCE FROM N.A.

REPAIN=C57BL/6J; TISSUE=Liver;

RX OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bonon H., Kondo S.,

RA OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bonon H., Kondo S.,

RA OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bonon H., Kondo S.,

RA OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bonon H., Kiyosawa H.,

RA Maraelli K., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli K., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Barelli K., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Barelli K., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanaj A., Kawaji H., Kawasawa Y., Kadzierski R.M., King B.L.,

RA Kanajaya A., Kurochkin I.V., Lee Y., Lenhard B. L.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Walls C.,

RA HIOZANE-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Harza A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.,

RA Manlysis of the mouse transcriptome based on functional annotation of
181 GRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGV 240
                                                                                                            GRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ICR; TISSUE=Brain;
MEDLINE=203479850, PubMed=10751414; DOI=10.1074/jbc.M002759200;
Liu H. Sugiura M., Nava V.E., Edsall L.C., Kono K., Poulton S.
Milstien S., Kohama T., Spiegel S.;
Molecular cloning and functional characterization of a novel
"mammalian sphingosine kinase type 2 isoform.";
J. Biol. Chem. 275:19513-19520(2000).
                                                                                                                                                                                                                                                     FAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL 384
                                                                                                                                                                                                                                                                                     241 FAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPFBEPL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thompson D., Pyne S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPH2 MOUSE STANDARD, PRT, 617 AA. 09JIA7; 091VA9; 09DBH6; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 65-UUL-2004 (Rel. 44, Last annotation update) 5phingosine kinase 2 (EC 2.7.1.-) (SK 2) (SPK 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Sphk2
                                                                                                               278
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Altausherg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci B., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKennan K.J., Malek J.A., Gunzafne P.H.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
A Rakealey R. W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGR 120
                                                                               300 RLFLAMQKGKHMDLDCPYLVHVPVVAFRLEPRNQRGVFSVDGELMVCEAVQGQVHPNYLW 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 VGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDBDFVLVLALLHSHLGSEMFAAPM 277
                                           RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETAIOKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 AA; 31684 MW; 2A0FDD51E64982C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC004112; AAH04112.2; -.
60; G0:0004143; Fidacylglycerol kinase activity; I
G0; G0:0007205; P:protein kinase C activation; IEA.
InterPro; IPR001206; DAGKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Pred. No. 9.3e-120;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  287 AA.
                                                                                                                                                                                    361 MVSGCVEPPSWKPQQMPPPEEPL 384
                                                                                                                                                                                                                                                     360 MVSGSSDSPSGRDSQRRPPPEPPI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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99.7%;
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD005043; DAGKc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPHK1 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=SPHK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286;
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***X TISSUBSET; PubMed=12477932; DOI=10.1073/pnas.242603899;
***REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

***A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

***A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

***A Ischul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Schuler G.D.,

***A Rachul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

***Raplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

***Raplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

***Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

***Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

***Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

***Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

***A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

***A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

***A Nilalon D.K., Muzny D.M., Sodergren B.D., Dickson M.C.,

***A Rhitting M.M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

***A Rhitting M.M., Touchman J.W., Green B.D., Dickson M.C.,

***A Rhitting M.M., Krzywinski M.I., Skalska U., Smailus D.E.,

***A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

***A Schnerch A., Schein J.S., Jones S.J.M., Marra M.A.,

***A Charly A. Schein J.E., Jones S.J.M., Marra M.A.,

***A Rhingosine 1-phosphate (SPP), a lipid mediator with both intra-

***A schningosine 1-phosphate (SPP), a lipid mediator with both intra-

***A schingosine 1-phosphate R.D., Able acts on D-erythro-

***A schingosine R.D., Able acts on D-erythro-

***A sching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.3%; Score 893; DB 1; Length 617;
39.9%; Pred. No. 3.3e-67;
tive 60; Mismatches 109; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATÂLYTIC ACTIVITY: Sphingosine + ATP = sphingosine 1-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF415448; AAF74125.1; ---
R EMBL; AF415214; AAL07500.1; ---
R EMBL; AF415214; AAL07500.1; ---
R EMBL; BC006941; BAB23694.1; ---
R EMBL; BC053737; AAH53737.1; ---
R MGD; MGI.1861380; Sphk2.
R MGD; GG:0005629; C:cytcos01; IEP.
GG; GG:0017050; F:D-erythro-sphingosine kinase activity; IDA.
GG; GG:0017050; F:D-erythro-sphingosine kinase activity; ISS.
GG; GG:0017050; F:D-erythro-sphingosine kinase activity; ISS.
GG; GG:0008481; F:sphinganine kinase activity; ISS.
R GG; GG:0006916; P:sphinganine-l-phosphate biosynthesis; NAS.
R GG; GG:0006669; P:sphinganine-l-phosphate biosynthesis; NAS.
R GG; GG:0006669; P:sphinganine-l-phosphate biosynthesis; NAS.
R InterPro; IPR007110; Ig-like.
R Pfam; PF00781; DAGK_cat; 1.
R PF0DOM; Vinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dihydrosphingosine, D-erythro-sphingosine and \tilde{\mathbf{L}}-threodihydrosphingosine.
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CONFLICT 252 252 N -> S (in Ref. 1).

CONFLICT 548 548 L -> F (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SIMILARITY: Contains 1 DAGKc domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65618 MW;
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70 GRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQV 129

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10 VLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEBL

Matches 192; Conservative

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TISSUE=Kidney,

TISSUE=Kidney,

TISSUE=Kidney,

Pubmed=12477932; DOI=10.1073/pnas.242603899;

Rausberg R.L., Felingold E.A., Grouve L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

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A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rans S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rans S.A., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rans V.J. Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ray Jones S.J., Marra M.A.,

Rans Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                     381 LHRSVSDLPLPLPQPALVSPGSPRPLPDLSLNGGGPELTGDWĠGAĠDAPLSPDPLLPSSP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 NALKTAQLSPIAEGPPEMPASSGFLPPTHSAPEASTWGPVDHLLPPLGSPLPQDWVTIEG 500
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||||| | ||:| |||||:||| 321 ARFTLGAVLGIASLHTYRGKLSYLPATTEPALPIPGHSLPRAKSELVLAPAPAATHSP 380
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                                                                                                                                         261 VGVDLLLINCSLLLCRGGSHPLDLLSVTLASGSRCFSFLSVAMGFLSDVDIHSERFRALGS
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Director MGC Project;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                               190 MRFTLGTFLRLAALRTYRGRLAYLPV-----
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dihydrosphingosine.
CATALYTIC ACTIVITY: Sphingosine + ATP = sphingosine 1-phosphate
  200
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                                                                                                                                                                               ------GRVG------GRVG-----
                                                                                                                                                                                                                                                                                                                                                                                                          ----SKTPAS-----SKTPAS------BVVVQQGPVDAHLVPLEEPVPSHWTVVPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                441 NAFKTAQLSPIAEGPSEMPASGLLPPIHNAPEASTWGPADHLLPPLGSPLPQDWVTIEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 VLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEEL
                                                                                                                                             Gaps
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MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
MEDILIBE-203479850; PubMed-10751414; DOI=10.1074/jbc.M002759200;
Liu H., Sugiura M., Nava V.E., Edsall L.C., Kono K., Poulton S.,
Milstien S., Kohama T., Spiegel S.;
"Molecular cloning and functional characterization of a novel
"Molecular cloning and functional characterization of a novel
mammalian sphingosine kinase type 2 isoform.";
J. Biol. Chem. 275:19513-19520(2000).
                                                                                                                    44.0%; Score 886.5; DB 2; Length 616;
            IEA.
                                                                                            616 AA; 65522 MW; BOD69D4894C69DB0 CRC64;
         GO, GO:0004143; F:diacylglycerol kinase activity, II
GO; GO:0007205; P:protein kinase C activation; IEA.
InterPro, IPR001206; DAGKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPH2_HUMAN STANDARD; PRT; 654 AM.
Q9NRAO; Q9BRN1; Q9HQQ2; Q9NWU7;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Sphingosine kinase 2 (EC 2.7.1.-) (SK 2)
                                                                                                                             Pred. No. 1.2e-66;
61; Mismatches 109;
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BC079120; AAH79120.1; -.
                                                                                                                               39.88;
                                            Pfam; PF00781; DAGK cat; 1.
ProDom; PD005043; DĀGKc; 1.
SMART; SM00046; DAGKc; 1.
                                                                                                                                        Matches 191; Conservative
                                                                               Hypothetical protein.
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                                                                                                                              Local Similarity
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TISSUBENCE FROM N.A. (ISOFORMS 1 AND 2).

TISSUB-29, and Lymph;

TISSUB-218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rischul S.F., Zeeberg B. Buetow K.H., Schamen C.M., Schuler G.D.,

A Rischul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

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A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wackernan R.J., Marker A.M., Gay L.J., Hulyk S.W.,

Raba S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Shevchenko Y., Boulfard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Browns A., Schein J.B., Jones S.J.M., Marra M.A.,

Broneration and initial analysis of more than 15,000 full-length human
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Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner Transards of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435 (2001).
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Search completed: June 15, 2005, 11:59:41 Job time: 177 secs
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                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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GRLSYLDAFVERASFYP -> PREBDSSYSSASACPLMTA
RSCPRAAASWPGSCPLLPQULALGFSRF1ODRVNGGGGRIG
SLTCRGHTQRTLBAPAREGGGSLFLKNINVF1CKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VSP 006217.
FEPALGLDLIINCSLILCRGGGHPLDLLSVTLASGSRCFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 VLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART: SM00046. DAGKC; 1.
Alternative splicing; ATP-binding; Kinase; Transferase.
Missing (in isoform 2 and isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.8%; Score 883.5; DB 1; Length 654; 39.6%; Pred. No. 2.3e-66; tive 62; Mismatches 107; Indels 127;
         Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005829; C:cytosol; IEP.
GO; GO:0005624; C:membrane fraction; IEP.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0017016; F:sphinganine kinase activity; NAS.
GO; GO:0008481; F:sphinganine kinase activity; NAS.
GO; GO:0006816; P:anti-apoptosis; NAS.
GO; GO:0006691; P:sphinganine-1-phosphate biosynthesis; NAS.
InterPro; IPR0071206; DAGKC.
InterPro; IPR0071206; DAGKC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRFTLGTFLRLAALRTYRGRLAYLPVG-RVGSKTPA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (in isoform 3).
/FIId=VSP_006218.
P -> S (in Ref. 2).
F73FFCEC930DA50F CRC64;
                                                                                                                                    IsoId=Q9NRA0-3; Sequence=VSP_006217, VSP_006218;
                                                                                                      IsoId=Q9NRA0-2; Sequence=VSP_006217;
                                                                      Sequence=Displayed;
                                                                                                                                                    SIMILARITY: Contains 1 DAGKc domain.
                                                                                                                                                                                                                                                                                                  EMBL; AF24547; AAF74124.1; --
EMBL; AL135701; CAB66636.1; --
EMBL; BC006161; AAH06161.1; --
EMBL; BC010671; AAH10671.1; --
EMBL; AK000599; BAA91280.1; --
Genew; HGNC:18859; SPHKZ.
H-InvDB; HIX0015297; --
MIM; 607092; --
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ProDom; PD005043; DAGKc; 1.
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hes 194; Conservative
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390
                                                           Name=1;
IsoId=Q9NRA0-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654 AA;
                                            isoforms;
                                                                                         Name=2;
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224
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                                      416 LHRSVSDLPLPQPALASPGSPEPLPILSLNGGGPELAGDWGGAGDAPLSPDPLLSSPP
                                                                                                                                                                                                        -----SPVVVQQ-----SPVVVQA-------GPVDAHLVPLEEPVPSHWTVVP
                                                                                                                                       476 GSPKAALHSPVSEGAPVIPPSSGLPLPTPDARVGASTCGPPDHLLPPLGTPLPPDW-VTL
                                                                                                                                                                                     254 DEDFVLVLALLHSHLGSEMFAAPMGRCAAGVWHLFYVRAGVSRAMLLRLFLAMEKGRHME
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June 15, 2005, 11:56:47; Search time 43 Seconds (without alignments) 666.634 Million cell updates/sec
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                                                                                                                                                                                                                                                 1 MDPAGGPRGVLPRPCRVLVL..........CVBPPSWKPQQMPPPEEPL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents AA:*
. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/6E_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
. /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                      513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                        US-10-642-289-2
2017
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                                                                                                                                                                                                            Title:
Perfect score:
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2005
2005
1920
1639
1627.5
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560
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                                                                                                                                                                                                                                                        Sequence:
                                                                                                                             Run on:
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		Description	1.4	2, App	20	Sequence 3, Appli	Sequence 21, Appl	98	Sequence 6, Appli	Sequence 15, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 328, App	Sequence 9, Appli	Sequence 12, Appl	Sequence 4, Appli	Seguence 14, Appl	Sequence 19, Appl	Sequence 20, Appl	788	6, 7	8	7,	128	13, App	Sequence 21, Appl	11, App
סו נוופ בסנפו פנסום מוזיוים	SUMMARIES	QI.	-60-	-516-2	US-09-949-016-7026	US-09-796-487-3	9	60-	-09-970-516-6	US-09-817-676A-15	US-09-796-487-2	US-09-796-487-1	US-09-796-487-4	US-09-796-487-5	US-09-205-258-328	US-09-796-487-9	US-09-817-676A-12	US-09-970-516-4	US-09-817-676A-14	9	-10-05	-09-20	US-09-796-487-6	-09-796-4	-09-796-487-7	-09-248-796A-	US-09-959-897-13	-09-959-897-2	US-09-959-897-11
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is defived by analysis of		Length	384	384	384	384	368	312	382	388	388	381	381	373	293	204	617	618	618	490	524	119	392	424	403	536	63		69
n naart	de	Query	100.0	99	99.4	99.4	95.2	81.3										43.8				22.	18.	-	17.2	16.	Ч	14.6	13.9
9 9 T F		Score	2017	2013	2005	2005	1920	1639	1629.5	1627.5	1627.5	1624.5	1624.5	1606.5	1538	935.5	894	883.5	883.5	260	519.5	453	375	357.5	346	330	295	295	280

Sequence 10, Appl	Sequence 18, Appl	Sequence 46720, A	Sequence 45874, A	Sequence 12, Appl	Sequence 20, Appl	Sequence 15, Appl	Sequence 23, Appl	Sequence 14, Appl		Sequence 9, Appli	Sequence 17, Appl	Sequence 45594, A	Sequence 33894, A	Sequence 49111, A	Seguence 16, Appl	Sequence 24, Appl	Sequence 264, App
US-09-959-897-10	US-09-959-897-18	US-09-270-767-46720	US-09-270-767-45874	US-09-959-897-12	US-09-959-897-20	US-09-959-897-15	US-09-959-897-23	US-09-959-897-14	US-09-959-897-22	US-09-959-897-9	US-09-959-897-17	US-09-270-767-45594	US-09-270-767-33894	US-09-270-767-49111	US-09-959-897-16	US-09-959-897-24	US-09-603-208A-264
4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
25	25	359	687	53	53	46	46	47	47	47	54	142	144	144	49	49	372
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249	249	239	239	234	234	216	216	201	201	184	184	180.5	180	180	170	170	162
28	53	30	31	32	160	3.6	35	36	37	80	39	40	4 1	4 2	. 4 . 6	44	45

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SEKYRRIGEMBFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVWHLFYVRAGVSRAMLL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDPAGGBRGVLPRPCRVLVLLINPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2017; DB 4;
100.0%; Pred. No. 4.7e-219;
tive 0; Mismatches 0;
                                                                  GENERAL INFORMATION:
APPLICANT: PITSON, Stuart M
APPLICANT: Brian, WATTENBERG W
APPLICANT: Brian, WATTENBERG W
APPLICANT: Richard, D'ANDREA J
APPLICANT: Richard, D'ANDREA J
APPLICANT: Anthew, VADAS A
ITILE OF INVENTION: SPHINGOSINE KINASE ENZYME
ILLE REPRENCE: PITSON-I
CURRENT APPLICATION NUMBER: US/09/959,897
CURRENT FILING DATE: 2001-11-13
FRIOR PILING DATE: 2000-05-12
FRIOR APPLICATION NUMBER: AU PQ 0339
FRIOR FILING DATE: 1999-05-13
FRIOR FILING DATE: 1999-05-13
FRIOR FILING DATE: 1999-05-13
FRIOR FILING DATE: 1999-05-13
FRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 384
                                   Sequence 2, Application US/09959897
Patent No. 6730480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 384; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-09-959-897-2
RESULT 1
US-09-959-897-2
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NAME/KEY: MISC_FEATURE
LOCATION: (1)._(384)
OTHER INFORMATION: SEQ ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, correspo
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| Sequence 3, Application US/09796487
| Sequence 3, Application US/09796487
| Sequence 3, Application US/09796487
| Pattent No. 68309104
| APPLICANT: Spiegel, Sarah
| TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
| TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
| TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
| CURRENT PRELICATION NUMBER: US/09/796,487
| CURRENT FILING DATE: 2000-03-03
| PRIOR FILING DATE: 2000-03-03
| PRIOR PILING DATE: 2000-05-05
| PRIOR PILING DATE: 2000-05-05
| SOFTAMBE: PatentIn version 3.1
| SEQ ID NO 3
| LENGTH: 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 SEKYRRIGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SEKYRRIGEMRFTIGTFIRAALRTYRGRIAYLPVGRVGSKTPASPVVVOOGPVDAHLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW
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                                                                                                                                                                                                                                                                                                                                                              Score 2005; DB 4;
Pred. No. 1.1e-217;
3; Mismatches 1;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
SEQ ID NO 7026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 MVSGCVEPPPSWKPQQMPPPEEPL 384
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.0%;
Matches 380; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                         US-09-949-016-7026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
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                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09970516
Patent No. 6610534
GENERAL INFORMATION
GEORGAT
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
CURRENT APPLICATION NUMBER: US/09/970,516
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
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Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
                                                                        360
                                                                                                301 RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFW 360
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  RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
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US-09-949-016-7026
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US-09-970-516-2
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TYPE: PRT
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ઠે 원 ò g ò 셤 ò g ઠે 셤 ò 셤 à 셤 Length 368;

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ORGANISM: Human
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OTHER INFORMATION: nding to amino acid residue 1 to 384 of Homo sapiens SPHK-1 of OTHER INFORMATION: nBank sequence Accession Number AAF73423.
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                        Gaps
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APPLICANT: SADA, Julie D.

APPLICANT: FYTEA, Henrik

TITLE OF INVENTION: SPHINGSINE-1-PHOSPHATE LYASE POLYPEPTIDES,

TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND

TITLE OF INVENTION: METHODS OF USE THEREFOR

FILE REFERENCE: 200116.40225,

CURRENT APPLICATION NUMBER: US,

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21

LENGTH: 368
                                                                                                                                                                                                                                                                                                        ;
0
                                            AUTHORS: Nava et al.
TITLE: Functional characterization of human spingosine kinase-1
JOURNAL: FEBS Lett.
VOLUME: 473
                                                                                                                                                                                                                                                                             Length 384;
                                                                                                                                                                                                                                                                                                        1; Indels
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Pred. No. 1.1e-217;
3; Mismatches 1;
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DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
                                                                                                                                              DATABASE ACCESSION NUMBER: AAF73423
DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 21, Application US/10053510; Patent No. 6830881
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.0%;
Matches 380; Conservative
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, ORGANISM: Homo sapiens
US-10-053-510-21
                                                                                                                                                                                         PUBLICATION INFORMATION:
                                                                                                       ISSUE: 1
PAGES: 81-84
DATE: 2000
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US-10-053-510-21
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                                                                                                                          61 VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT
                                                                                                                                                            NCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGT
                                                                                                                                                                           PIRLAALRIYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDED
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                                                                    1 VLVILNPRGGKGKALQLFRSHVQPLLABABISFTLMLTERRNHARELVRSEELGRWDALV
                                                     17 VLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALV
                                                                                                          77 VMSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT
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99.7%; Pred. No. 1.8e-176;
iive 1; Mismatches 0;
95.2%; Score 1920; DB 4; 99.7%; Pred. No. 4.1e-208; ive 1; Mismatches 0;
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Matches 311; Conservative
                Best Local Similarity 99.7
Matches 367; Conservative
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US-09-817-676A-15
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US-09-796-487-2
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APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31677
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
312
               181 PDEDFVLVLALLHSHLGSEMPAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHM 240
                                                   372
                                                                 241 EYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSW 300
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                                                                                                                                                                                   US-09-970-516-6; Sequence 6, Application US/09970516; Patent No. 6610534
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.4%;
Matches 308; Conservative 34
                                                                                                                                 301 KPÓOMPPPEEPL 312
                                                                                                      373 KPQQMPPPEEPL 384
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Sequence 15, Application US/09817676A
Patent No. 6800470
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takafumi

RESULT 8 US-09-817-676A-15

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Sequence 2, Application US/09796487

Patent No. 6830916

Batent No. 6830916

Batent No. 6830916

GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah

TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REFERENCE: 07320001aa (2033957-0001)

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: US 60/186,532

PRIOR APPLICATION NUMBER: US 60/186,532

PRIOR APPLICATION NUMBER: US 09/530,868

PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 17
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TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning, TITLE OF INVENTION: Expression and Methods of Use Thereof FILE REPERENCE: 00170/HG CURRENT APPLICATION NUMBER: US/09/817,676A CURRENT FILING DATE: 2001-03-26 PRIOR PILIATION NUMBER: US 60/194,318 PRIOR FILING DATE: 2000-04-03 NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 15 LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
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80.7%; Score 1627.5; DB 4; Length 388;
Best Local Similarity 81.4%; Pred. No. 5.2e-175;
Matches 307; Conservative 33; Mismatches 36; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSUE: 37
PAGES: 23722-23728
DATE: 1998-09-11
DATABASE ACCESSION NUMBER: AAC61698
DATABASE ENTRY DATE: 1998-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE: murine sphingosine kinase
JOURNAL: J. Biol. Chem.
VOLUME: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 EPPPSWKPQQMPPPEEP 383
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mus musculus
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FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1): .(381)
COTHER INFORMATION: SEQ ID NO 1 is the peptide sequence of SPHKIa in Figure 1, corres
OTHER INFORMATION: ponding to amino acid residue 124 to 504 of SPHKIa of GenBank seq
OTHER INFORMATION: Donding to amino acid residue 124 to 504 of SPHKIa of GenBank seq
OTHER INFORMATION: Usuance Accession Number AAC61697: SEQ ID NO 1 is equivalent to SEQ
OTHER INFORMATION: ID NO 4 that is the amino acid sequence of mSPHKIa in Figure 3.
PUBLICATION INFORMATION:
AUTHORS: Kohama et al.
TITLE: Molecular cloning and fuctional characterization of murine sphingosin
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                                                                                                                                                                                                                                                                                                                                                                                                  TITLE: kinase
JOURNAL: Journal of Biological Chemistry
VOLUME: 237
                         09/230,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSUE: 37
PAGES: 23722-23782
DATE: 1998
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)..(504)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)..(504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/09796487; Patent No. 6830916; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 EPPPSWKPQQMPPPEEP 383
  PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: US 05
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAPSGRDSRRGPPPEEP
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                                                                                                                            LENGTH: 381
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-796-487-4
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 388
TYPE: PRT
ORGANISM: Mus Musculus
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(388)
OTHER INFORMATION: SEQ ID NO 2 is the peptide sequence of SPHKIb in Fig. 1, corresponding to amino acid residue 1 to 388 of SPHKIb of GenBank sequency
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Kohama et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09796487

Patent No. 6830916
GENERAL INFORMATION:
Spiegel, Sarah
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487

CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,532
                                                                                                                                                                                                                                                                          TITLE: Molecular cloning and fuctional characteriation of murine sphingosine IITLE: kinase JOURNAL: Journal of Biological Chemistry VOLUME: 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

80.7%; Score 1627.5; DB 4
Best Local Similarity 81.4%; Pred. No. 5.2e-175;
Matches 307; Conservative 33; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                         DATABASE ACCESSION NUMBER: AAC61698
DATABASE ENTRY DATE: 1998-09-26
PELLEVANT RESIDUES: (1)..(388)
PUBLICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATABASE ACCESSION NUMBER: AAC61698;
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (1)..(388)
US-08-796-487-2
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PAGES: 23722-23728
DATE: 1998
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US-09-796-487-1
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RESULT 13
US-05-205-258-328
; Sequence 328, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
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DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (132)..(504)
      US-09-796-487-5; Sequence 5, Application US/09796487; Patent No. 6830916; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 PSWKPQQMPPPEEP 383
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360 SGRDSRRGPPFEEP 373
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                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(381)
OTHER INFORMATION: SEQ ID NO 4 is the peptide sequence of mSPHKla in Figure 3, corre
OTHER INFORMATION: SEQ ID NO 4 is the peptide sequence of SPHKla of GenBank se
OTHER INFORMATION: quence Accession Number AF068748. SEQ ID NO 4 is equivalent to SE
OTHER INFORMATION: Q ID NO 1 that is the amino acid sequence of SPHKla in Figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
AUTHORS: Kohama et al.,
ITTLE: Molecular cloning and functional characterization of murine sphingosine
ITTLE: kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 EELGHWDALAVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGSGGNALAASVNHYAGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 EQYTNEDLLINCTLILCRRRLSPWNLLSLHTASGLRLYSVLSLSWGFVADVDLESEKYRR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGFVDAHLVPLEEPVP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 QKGKHMELDCPYLVHVPVVAPRLEPRSQRGVFSVDGELMVCEAVQGQVHPNYLMMVCGSR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQVINEDLLINCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRR 186
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TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of (FILE REFRENCE: 0732001ag (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ 1D NOS: 17
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 PRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL: Journal of Biological Chemistry
VOLUME: 273
ISSUE: 37
PAGES: 23722-23728
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DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)..(504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: 1996
DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDNES: (124).. (504)
PUBLICATION INFORMATION:
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Matches 306; Conserv
                                                                                                                                                                                                                                    LENGTH: 381
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US-09-796-487-4
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RESULT 12

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TYPE: PRT
ORGANISM: Mus musculus
PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)._(373)
OTHER INFORMATION: SEQ ID NO 5 is the peptide sequence of Mouse SPHKIa in Fig. 2, co
OTHER INFORMATION: Tresponding to amino acid residue 131 to 504 of SPHKIa of GenBank
OTHER INFORMATION: sequence Accession Number AAC61697.
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APPLICANT: Spiegel, Sarah

TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of PILE REPERBUCE: 07320001aa (2033957-0001)

CURRENT APPLICATION NUMBER: US/09/796,487

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: US 60/186,532

PRIOR APPLICATION NUMBER: US 09/530,868

PRIOR PILING DATE: 2000-03-03

PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1

SEQ ID NO 5.
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79.6%; Score 1606.5; DB 4;
Best Local Similarity 81.0%; Pred. No. 1.2e-172;
Matches 303; Conservative 34; Mismatches 36;
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
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us-10-642-289-2.rai

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CURRENT FILING DATE: 1998-0-04

EARLIER FILING DATE: 1997-06-06

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assembling sequences from s D31133, AA232791, W63556, AA FEATURE:
CTHER INFORMATION: Putative kinase sequence obtained by assembling sequences from the INFORMATION: everal human ESTS (accession numbers D31133, AA232791, W63556; OTHER INFORMATION: 081152 and AA026479).
NAME/KEY: MISC\_PEATURE
COCATION: (1)...(204); OTHER INFORMATION: Corresponding to peptide sequence Putative Human in Figure 2. US-09-796-487-9 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT APPLICATION NUMBER: US 60/186,532
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR PRICATION NUMBER: US 09/530,868
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 9
LENGTH: 204 ö 331 240 NAME/KEY: SITE
CATION: 136)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-328 92 MERPDWETALQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMN 151 LLSIHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA 211 271 9 1 MERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYXQVINEDLLINCTLLLCRRLLSPWN 212 YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSE 272 MFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEP Gaps 332 KÖGKGMFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL 384 241 KDGKGVFAVDGELMVSEAVQGQVHPNYFMWVSGCVEPPPSWKPQQMPPPEEFL 293 . 0 Length 293 1; Indels 76.3%; Score 1538; DB 4; 99.3%; Pred. No. 4.4e-165; iive 1; Mismatches 1; EARLIER FILING DATE: 1997-06-06
FARLIER PILING DATE: 1997-06-06
FARLIER PILING DATE: 1997-12-18
FARLIER PILING DATE: 1997-12-18
FARLIER APPLICATION NUMBER: 60/092, 921
FARLIER PILING DATE: 1998-07-15
FARLIER PILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 328
LENGTH: 293 EARLIER APPLICATION NUMBER: 60/048,878 Sequence 9, Application US/09796487 Patent No. 6830916 Query Match 76.3 Best Local Similarity 99.3 Matches 291; Conservative TYPE: PRT ORGANISM: Homo sapiens FEATURE: TYPE: PRT ORGANISM: Unknown RESULT 14 US-09-796-487-9 152 셤 ઠ ઠે 유 ò 셤 Š 쉽 ò

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APPLICANT: Kohama, Takafumi
APPLICANT: Kohama, Takafumi
APPLICANTON: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REPERENCE: 00170/HG
FILE REPERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
                                                                                                                       INPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALVVMSG
                                                                               LINPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALVVMSG
                                                                                                                                                                                                                                            141 LLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRL
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                                           Gaps
                                         Indels 137;
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39.9%; Pred. No. 8.9e-92;
tive 61; Mismatches 108; Indels 120;
Query Match 46.4%; Score 935.5; DB 4; Length 204; Best Local Similarity 58.1%; Pred. No. 3.2e-97; Matches 198; Conservative 4; Mismatches 2; Indels 137,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 YVPVVAFRLEPKDGKGMFAVDGELMVSEAVQGQVHPNYFWM 361
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SEQ ID NO 12
LENGTH: 617
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US-09-817-676A-12
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Best Local Simil
Matches 192; C
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  Query Match
Best Local (
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- nucleic search, using sw model OM nucleic Run on:

June 17, 2005, 02:31:28; Search time 5404 Seconds (without alignments) 10804.688 Million cell updates/sec

US-10-642-289-1 1205 1 gaattcggcacgaggagccg......gatctagagtcgacctgcag 1205

Title: Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4708233 segs, 24227607955 residues Searched:

9416466

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

gb\_sts:\* gb\_sy:\* gb\_un:\* gb\_vi:\* gb htg: \*
gb\_ov: \*
gb\_ov: \*
gb\_ov: \*
gb\_bt: \*
gb\_pt: \*
gb\_pt: \* 110: 111: 14:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	BD267580 Sphingosi		AF200328 Homo sapi	BD270642 Regulator	AF266756 Homo sapi	- AX127641 Sequence	BD157644 Primer fo	AX879091 Sequence	AK022402 Homo sapi	_	BD158407 Primer fo	AX880488 Sequence	AK023393 Homo sapi	BC008040 Homo sapi	BC014439 Homo sapi	AK122781 Homo sapi	AF238083 Homo sapi	BD192995 207 human	CQ821991 Sequence
ID	RD267580	AR533266	AF200328	BD270642	AF266756	AX127641	BD157644	AX879091	AK022402	BC030553	BD158407	AX880488	AK023393	BC008040	BC014439	AK122781	AF238083	BD192995	CQ821991
DB	٧	9	σ	9	σ	9	y	9	6	σ	9	9	σ	σ	σ	σ	σ	9	9
% Query Match Length	1205	1205	1173	1573	1693	1719	1821	1821	1821	2174	1772	1772	1772	1815	2133	2238	1783	1533	1533
% Query Match	1000	100.0	97.3	97.0	97.0	97.0	97.0	97.0	97.0	97.0	96.8	96.8	96.8	96.7	96.7	9.96	96.5	95.4	95.4
Score	1205	1205	1173	1168.6	1168.6	1168.6	1168.6	1168.6	1168.6	1168.6	1167	1167	1167	1165.4	1165.4	1163.8	1162.6	1149.4	1149.4
Result No.	-	10	; (*)	4	ď	9	7	•	0	10	11	12	13	14	15	16	17	18	19

20 1147 95.2 1155 6 AR382730 21 1141.8 94.8 1155 12 AY335568 22 1141.8 94.8 1155 12 BY007458 24 1141.4 94.7 1600 6 AX224379 25 1140.4 94.6 1869 6 CQ776506 26 1140.4 94.6 1869 9 BC099419 27 1138.8 94.5 2502 9 AK095578 28 1096 91.0 1428 9 HSA45504 29 991.2 87.3 2 015 9 AR095578 31 774.8 64.3 1183 9 BC04412 32 774.4 64.3 1337 9 BC06412 34 773.6 64.2 1687 10 BC037710 35 773.6 64.2 1687 10 BC037710 37 763.6 63.1 1948 6 AX224381 37 763.6 63.1 1842 10 AB049571 41 760.6 63.1 1842 10 AB049571 42 760.6 63.1 1895 10 AB049573 44 760.6 63.1 2648 10 AB049573 45 757.6 62.9 1815 6 AX38732	AR382730 Sequence	AX127642 Sequence	AY335568 Synthetic	BT007458 Synthetic	AX224379 Sequence	CQ776506 Sequence	BC009419 Homo sapi			AB046025 Macaca fa	BC004112 Homo sapi		AC090699 Homo sapi	BC037710 Mus muscu	AY278525 Homo sapi	AC068145 Homo sapi	AX224381 Sequence	BC081738 Rattus no	AC021196 Homo sapi	AB049573 Rattus no	AB049572 Rattus no	AB049571 Rattus no	AB049574 Rattus no	AB049575 Rattus no	AR382732 Sequence	AX287137 Sequence	
20 1147 95.2 1155 22 1141.8 94.8 1155 23 1141.8 94.8 1155 24 1141.4 94.7 1600 25 1140.4 94.6 1869 27 1138.8 94.5 2502 28 1096 91.0 1428 30 854.8 10.9 1428 31 774.8 64.3 138379 32 774.4 64.3 138379 33 773.6 64.2 1864 34 773.4 64.2 1867 35 773.6 64.2 1867 36 773.6 63.1 1895 37 76.6 63.1 1895 41 760.6 63.1 1895 42 760.6 63.1 1895 43 760.6 63.1 1895 44 750.6 63.1 1895 44 750.6 63.1 1943	AR382730	AX127642	AY335568	BT007458	AX224379	CQ776506	BC009419	AK095578	HSA245504	AB046025	BC004112	CQ724590	AC090699	BC037710	AY278521S5	AC068145	AX224381	BC081738	AC021196	AB049573	AB049572	AB049571	AB049574	AB049575	AR382732	AX287137	•
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22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 22220 2220 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 2220 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 22200 2200 2200 2200 2200 2200 2200 2200 2200 2200 2200 2200 2200 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 2000 200	01		01	٠,	0,		٠,	٠.													_						
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## ALIGNMENTS

linear PAT 17-JUL-2003		co 1205) Wattenberg, B.W., Xia, P., DGandrea, R.J., Gamble, J.R. Alase		Mammalian 24 - DEC-2002 12 - MAY-2000 JP 2000618434 12 - MAY-2000 JP 2000618434 13 - MAY-2000 JP 2000618434 13 - MAY-1999 AU PQ 1504 PI RT MAXWELL PITSON, BRIAN WOLFF WATTENBERG, PU XIA PI ,RICHARD JENNIFER RUTH GAMBLE, MATHEW ALEXANDER VADAS 115/09, A61X31/711, A61X38/43, A61X38/55, A61X39/395, A61X39/395, PC A61X64 NO, A61P9/10, A61P11/06, A61P25/00, A61P25/28, A61P29/00, PC A61X48 NO, A61P9/10, A61P11/06, A61P25/00, A61P25/28, A61P29/00, PC A61P3/10, A61P3/10, A61P3/40, A61P3/40, A61P3/48, A61P3/48	
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DNA		а, Р., D	-2002; LTD	1000618434 'BRIAN WOLFF WATTENN MBLE, MATHEW ALEXAND) A61K38/43, A61K38/55 10, A61P11/06, A61P25, /40, C12N5/00, C12N5/ 53, G01N33/577, C12N1:	<u>.</u>
đq		Χį	DEC	14 70LF 13,A 13,A 13/0 15/0 19/1	Eied DNA."
1205 bp	<b>6</b> 0	g, B.W.,	A 1 24- SEARCH	11-A/1  JP 2000618434  AU  FO 0339,08  TISON, BRIAN WOLFF W  H GAMBLE, MATHEW AL  711, A61K38/43,A61K  11P9/10,A61P11/06,A  77K16/40,C12N5/00,C  Kinase  Location/Quali	ifiers identifiers momic I
BD267580 Sphingosine kinase. BD267580	BD267580.1 GI:33077348 JP 2002543831-A/1. unidentified unidentified unidentified unclassified.		Percent of 2002543831-A 1 24-DEC-2002; JOHNSON AND JOHNSON RESEARCH PTY LTD	OS Mammalian PN JP 20025331-A/1 PD 24-2002 PP 12-MAY-2000 PP 24-DEC-2002 PR 12-MAY-1999 PR 13-MAY-1999 PR 13-MA	Location/Qual. 1205 /organism="um/mol_type="g"/db_xref="ta
RESULT 1 BD267580 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	JOURNAL	COMMENT	FEATURES source

Qy         1021 AGCCCAAGGATGGGAAAGGTATGTTTGCAGTGGAATTGATGGTTAGCGAGGCCG         1080           Db         1021 AGCCCAAGGATGGAAAGGTATGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCG         1080           Qy         1081 TGCAGGCCAGGTGCACCCAACTACTTCTGGATGGGGATTGATGGTGGAGCCCCGC         1140           Db         1081 TGCAGGCCAGGTGCACCCAAACTACTTCTGGATGGTCAGCGGTGGAGCCCCCGC         1140           C         1141 CCAGCTGGAAGCCCCAGCAGATGCCCCCCAGAAGAGCCCCTTATGATCTAGAGTCGACC         1140           Db         1141 CCAGCTGGAAGCCCCAGCAGAACTACTTCTGGATGGTCGAGGCCCCCGC         1140           Db         1141 CCAGCTGGAAGCCCCAGCAGAACACCCCCCAGAAGAGCCCTTATGATCTAGATCGACC         1200           Qy         1201 TGCAG 1205           Db         1201 TGCAG 1205	RESULT 2 AR533266 LOCUS DEFINITION Sequence 1 from patent US 6730480. ACCESSION AR533266 ACCESSION AR533266 VERSION KEYNONES UDAINOWN. ORGANISM UDAINOWN. ORGANISM UDAINOWN. ORGANISM P. D'Andrea,R.J., Gamble,J.R. AUTHORS Pitson,S.M., Wattenberg,B.W., Xia,P., D'Andrea,R.J., Gamble,J.R. AUTHORS SOURCE JOURNAL Patent: US 6730480-A 1 04-MAY-2004; FEATURES SOURCE ACCESSION ACCESSION AR533266 ACCESSION AR533266 ACCESSION AR533266 ACCESSION AR533266 ACCESSION AR533266 ACCESSION A	Query Match
Query Match         100.0%;         Score 1205;         DB 6;         Length 1205;           Best Local Similarity 100.0%;         Pred. No. 9.6e-218;         O 6.5 Ength 1205;         O 6.5 Ength 1205;           Matches 1205;         Conservative 0;         Mismatches 0;         Indels 0;         Gaps 0;           Qy         I GAATTCGGCACGAGACCCGGGGTCAGAGTTATGGATCCAGCGGCACCCCCGGGGCAGGGC 60         O 6.1 TGCTCCCCCCCCCGCGGGTCAGAGTTATGGATCAGCGGCAGCGCAAGGGCAAGG 120           Qy         6.1 TGCTCCCCCCCCCCGCGGGTGGTGGTGGTGATGACCCGGCGCAAGGGCAAGG 120         D 6.1 TGCTCCCGCGGCCCGGGGTCAGGGCTGAGGCTGAACCCGCGCGCAAGGGCAAGGGAAGGGAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGAGCAAGGCAAGAGCAAGACACAGGCACAGAGGCACAGAGCACAGAGCACAGAGCACAGAGCACAGAGCACAGAGCACAGAGCACAGAGCACAGAGAAGA	181   CGCTGATGCTCACTGGGGGAACCACGGGGGGGGTGGTGGTGCGGTCGGAGGGGGG 240	19

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                                            Moretti, P.A.B., Xia, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TGCCGCGTGCTGCTGCTGCTGAACCCGCGCGGCGGCGAAGGGCAAGGCCTTGCAGCTCTTC
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pitson, S.M., D'Andrea, R.J., Vandeleur, L., Morett Gamble, J.R., Vadas, M.A. and Wattenberg, B.W.
Direct Submission
Submitted (129-0CT-1999) Human Immunology, IMVS, Adelaide, SA 5000, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.3%; Score 1173; DB 9; L. llarity 100.0%; Pred. No. 1.1e-211; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pitson, S.M., D'andrea, R.J., Vandeleur, L., Moretti, P.A., Xia, P., Gamble, J.R., Vadas, M.A. and Wattenberg, B.W.
Human sphingosine kinase: purification, molecular cloning and characterization of the native and recombinant enzymes
Biochem. J. 350 Pt 2, 429-441 (2000)
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A61P25/22,A61P25/28,A61P27/00,A61P29/00,A61P29/00,A61P31/10,
A61P31/00,A61P35/00,A61P35/02,A61P37/08,C07K14/47,C07K16/18,
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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E 1 (bases I to 1573)

E 1 (bases I to 1573)

Saimzan, O., Tang, T.Y., Yue, H., Hillman, J.L., Baughn, M.R., Azimzai, Y., Lu, D.A.M. and Young, J.A.

Azimzai, Y., Lu, D.A.M. and Young, J.A.

Regulators of intracellular phosphorylation

Patent: JP 2002538827-A 5 19-NOV-2002;

INCYTE PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 200253887-A/5

PP 19-NOV-2002

PR 18-MAR-1999 US 60/125593,20-MAY-1999 US 60/135049 PR 18-MAR-1999 US 60/125593,20-MAY-1999 US 60/143188

PI OLGA BANDMAN, TOM Y TANG, HENRY YUE, JENNIFER L HILLMAN, MARIAH R PI BAUGHN,

PI YALDA AZIMZAI, DYING AINA M LU, JANICE AU YOUNG PC.
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CIZNIS/09, AGIK38/46, AGIK45/00, AGIP1/16, AGIP1/18, AGIP3/10 PC
, AGIP7/04, AGIP7/06,
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KGVPAVDGELAVSEAVQGQVHPNYFWNVSGCVEPPPSWKPQQMPPPEEPL"
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Pred. No. 6.9e-211;
0; Mismatches 9;
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99.2%;
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Best Local Similarity 99.2
Matches 1174; Conservative
                                  polyA_signal
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GSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAP
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Helendez, A.J., Carlos-Dias, E., Gosink, M., Allen, J.M. and Takacs, L. Human Sphingosine Kinase, Molecular Cloning, Functional Characterisation and Tissue Distribution
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2 (bases 1 to 1693)
Melendez, A.J., Carlos-Dias, E., Gosink, M., Allen, J.M. and Takacs, L.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                      1004 CGGGAGTGTCTCGTGCCCATGCTGCGCCTCTTCCTGGCCATGGAGAGAGGCAGCATA
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         GCCCGGTAGATGCACACCTTGTGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGG
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Submitted (11-MAY-2000) Department of Molecular and Cellular
Biology, Jouveinal Parke-Davis, 11-13 rue de la Loge, Fresnes
94265, France
                                                                                                                                                                                                                                                                                                                                                                        1244 GGAAGCCCCAGCAGCACCACCGCAGAAGACCCTTATGACC 1286
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Homo sapiens sphingosine kinase
AP266756
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		RESULT 7  BD157644  BD15764  BD157644  BD15764  BD157644  BD15764  BD157644  BD15764  BD177C  BD17C  BD
Qy         967 TGGAGTATGAATGCCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCGGCTTGGAGCCCA         1026           bb         1204 TGGAGTATGAATGCCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCGGCTTGGAGCCCA         1263           Qy         1027 AGGATGGAAAGGTATGTTGCAGTGGATGGTCGCTTCCGCTTGGAGCCCTACGAGCCCTACGAGGCCGTGCAGG         1086           Db         1264 AGGATGGGAAAGGTGTTTGCAGTGGATGGGGAATTGATGGTGAGGCCGTGCAGG         1333           Qy         1087 GCCGGGGAAAGGTACTTCTGGATGGTGGGGGATTGGTGAGGCCCCCGCCCAGCGTTATGATGGTGAGGCCCCCAGCCCCAGGAGGTTGCTCAGCGGTTGCGTGAGGCCCCCAGCCCCAGGTTGCTATGATGCTCAGCGGTTGCGTGAGGCCCCAGAGCTTATGATCGTTAGGAGCCCCCAGCCCCAGAACTACTTTTGATGATCCTTATGATCCTTATGATCCTTATGATC         1146           Qy         1147 GGAAGCCCCAGCAGAAGTGCCCCAGAAGAGCCCTTATGATC         1189           1184 GGAAGCCCCAGCAGAAGACCCCAGAAGAGCCCTTATGATC         1189           1184 GGAAGCCCCAGCAGAAGACCCCAGAAGAGCCCTTATGACC         1426	RESULT 6  AX127641  DEFINITION Sequence 1 from Patent W00131029.  DEFINITION Sequence 1 from Patent W00131029.  AX127641  AX12764  AX127641  AX127	127 AGCTCTTCCGGAGTCACGTGCAGCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGA

1086 1446

1026 1386

1326

996

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LTAFSVLSLANGFIADVDLESEKYRRLGEMFTLGFTEIRLARLTTARGRLAF
GSKTPASPVVVQQGPVDAHLVPLEBEVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAP
MGRCAAGVMHLPYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEFKDG
KGVFAVDGELMVSEAVQGQVHPNYFMWVSGCVEPPPSWKPQQMPPPEEPPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primers for synthesising full-length cDNA and their use
Patent: BP 1074617-A 13996 07-FEB-2001;
Research Association for Biotechnology (JP)
Location/Qualifiers
1. 1821
//organism="Homo sapiens"
//mol_type="unassigned DNA"
//db.xref="taxon:9606"
393. 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 17-DEC-2003
1087 GCCCGGTAGATGCACACCTTGTGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGG 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                           TGABGTATGAATGCCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCA
                                                                                                                                                                                                                                     1207 FGTTTGCTGCACCCATGGGCCGCTGTGCAGCTCATGCATCTGTTCTACGTGGGGG
                                                                                                                                                                     AGGATGGGAAAGGTATGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGG
                                                                                                                                                                                                                                                                                                                                          GCCAGGTGCACCCCAAACTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCT
                                                                                         TGTTTGCTGCACCCATGGGCCGCTGTGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGG
                                                                                                                                                    Gaps
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97.0%; Score 1168.6; DB 6; Length 1821;
Best Local Similarity 99.2%; Pred. No. 6.8e-211;
Matches 1174; Conservative 0; Mismatches 9; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                      1507 GGAAGCCCCAGCAGCACCGCCAGAAGACCCCTATGACC 1549
                                                                                                                                                                                                                                                                                                                                                                                                       GGAAGCCCCAGCAGATGCCACCACAGAAGAGCCCTTATGATC 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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AX879091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX879091.1 GI:40033827
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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    PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SALTO,
PI JUNICHI YAWAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC
CIZNIS/09, CO7K14/47, CO7K16/18, CIZNI/15, CIZNI/19, CIZNI/21, CIZNS/ PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACTCTGGGCACTTTCCTGCGTCTGGCAGCTTGCGCACTTACCGCGGCCGACTGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                 ||||| GCACCGGGAGCCCCGGGTCGAGGTTATGGATCCAGCGGCGCCCCCGGGGCGTGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                              CGCGGCCTGCCGCGTGCTGGTGCTGAACCCGCGGCGGCGAAGGGCAAGGCCTTGC
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Pred. No. 6.8e-211;
0; Mismatches 9;
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                                                                                                                                                                                                          1. .1821
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Best Local Similarity 99.2%;
Matches 1174; Conservative
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426	OS         1147         GRANGCCCAGCAGATGCCACCAGAAGAGCCTT           CFG         1147         GRANGCCTTGC         126         120         GRANGCCTTGC         120         120         GGAAGGCCAGCAGATGCCACCAGCAGAAGACCCTTGC         186         150         GGAAGGCCTAGCAAGACCTTGC         186         150         GGAAGCCCTAGCAAGAAGACCTTGC         186         150         GGAAGCCCTAGCAAGAAGACCTTGC         186         150         GGAAGCCCTAGCAAGAAGACCTTGC         186         150         GGAAGAAGAAGAAGAAAGAAAAAAAAAAAAAAAAAAA	186 RESULT 9 AK022402 546 LOCUS	246	306 KEYWORDS 306 SOURCE ORGANISM 666	366 REFERENCE AUTHORS 726	CTATGAGCAGGTCACCAATG 426 Sekine, M., Obayashi, M., Nishir, T., Shibs Shibs Ships Shi	486 846	546 906	909	666 1026	726 1086	786 1146 TITLE	946 JOURNAL PUBMED 1206 REFERENCE	906 AUTHOKS 1266	966 1326	1026 REFERENCE AUTHORS AUTHORS 1386 TITLE	1086 COMMENT
367 GGCAGCGGGAGCCGCGGGTCGAGGTTATGGATCCAGCGGGCGG	67 CGCGGCCCTGCCGCGTGCTGCTGAACCCGCGGGCGGCAGGCA	127 AGCTCTTCCGGAGTCACGTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGA 	187 TGCTCACTGAGCGGCGGAACCACGCGGGGAGCTGGTGCGGTCGGAGCTGGGCCGCT 	247 GGGACGCTCTGGTGGTCATGTCTGGAGACGGGCTGATGCACGAGGTGGTGAACGGGCTCA 	307 IGGAGCGGCCTGACTGGGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCT	367 CTGGCAACGCGCTGGCAGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATG	427 AAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGGCTGCTGCTGTCACCATGAACC	487 IGCIGICICIGCACACGGCIICGGGGCIGCGCCICITCICIGIGGTCAGCCIGGCCIG	547 GCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATGGCGGTCTGGGGGAGATGCGCT	607 TCACTCTGGGCACTTTCCTGCGTCTGGCAGCCTTGCGGCACTTACCGCGGCCGACTGGCTTT	667 ACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCCTCCCCGGTTGTGGTCCAGGGGGGT	727 GCCCGGTAGATGCACACTTGTGCCACTGGAGGGCCCGTGGCCCTCTCACTGGACAGTGG	787 IGCCCGACGAGGACTITIGIGCTAGTCCTGGCACTGCACT	847 TGTTTGCTGCACCCATGGGCGGCTGTGCAGCTGGCGTCATGTTCTACGTGCGGGGGGGTCTTGTTCTACGTGCGGGGGGGG	907 CGGGAGTGTCTCGTGCCATGCTGCGCCTCTTCCTGGCCATGGAGAGGGCAGGCA	967 TGGAGTATGAATGCCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCA 	1027 AGGATGGGAAAGGTATGTTTGCAGTGGAATGGGGAATTGATGGTTAGCGAGGCCGTGCAGG
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Suki,T., Sugiyama,T., Irie,R.,
Nagai,K., Kimura,K., Makita,H.,
Nhibahara,T., Tanaka,T., Tanaka,T.,
Iwayanagi,T., Wagatsuma,M.,
Iwayanagi,T., Wagatsuma,M.,
Yoku,Y., Kodaira,H., Kondo,H.,
Yokoi,T., Frunya,T.,
Yara,K., Katsuta,N., Sato,K.,
Kimata,M., Watanabe,M.,
No,Y., Takahashi-Fujii,A.,
No,Y., Takahashi-Fujii,A.,
Natsunawa,H., Satch,N., Takahashi-Fujii,A.,
Natsunawa,H., Satch,N., Takahashi-Fujii,A.,
Natsunawa,H., Watanabe,T.,
Migaki,H., Watanabe,T.,
Nigaki,H., Watanabe,T.,
Nigaki,H., Watanabe,T.,
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Nigaki,H., Watanabe,T.,
Nigaki,H., Watanabe,T.,
Nimori,Y., Komiyama,M.,
Nimori,Y., Komiyama,M.,
Nimori,Y., Komiyama,M.,
Nimori,Y., Komiyama,M.,
Natana,A., Hikiji,T., Kobatake,N.,
Natsu,T., Matsumtra,K.,
Sasaki,M., Togashi,T.,
Assaski,M., Togashi,T.,
Aston, Isogai,T. and Sugano,S.
Nakagawa,K., Okumura,K.,
Nakagawa,K., Okumura,K.,
Nakagawa,T., Wanspilta,R.,
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Nakaton,T., Taka,T., Taka,T.,
Nakaton,T., Taka,T., Taka,T.,
Nakaton,T., Taka,T., Taka,T.,
Nakaton,T., Tak i, Helix Research Institute, isarazu, Chiba 292-0812, Japan 438-52-3975, Fax:81-438-52-3986) supported by Ministry of Japan; CDNA full insert r Biotechonlogy; cDNA library r sequencing and clone selection: by Japan Key Technology Center NA linear PRI 30-JAN-2004 MAMMA1002268, moderately inase (SPHKIa) mRNA. yama,T., Otsuki,T., Suzuki,Y., Shiratorii,A., Sudo,H., Kodaira,H., Kondo,H., Ishida,S., Murakawa,K., Kimura,K., Murakami,K., Oto,J., Wakamatsu,A., a; Vertebrata; Euteleostomi; iini; Hominidae; Homo. TTATGATC 1189 TTATGACC 1549 nce).

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 2174)

Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschull,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max.S.I., Wang,J., Heich,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleron,M., Soares,M.B., Bonddo,M.F., Casavant,T.L.,
Stapleron,M., Soares,M.B., Bonddo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mallahy,S.J., Gunatane,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Young,A.C., Shevchenko,Y.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Butterfield,Y.S., Kzzywinski,M.I., Skalska,U., Smailus,D.E.,
Butterfield,Y.S., Kzzywinski,M.I., Skalska,U., Smailus,D.E.,
Konnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
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Homo sapiens sphingosine kinase 1, mRNA (cDNA clone MGC:40267
IMAGE:5213270), complete cds.
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0; Mismatches 9; Indels 0;
                                                                                                                                                                                                          /note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                  product"
                                                                                                                                             /clone="MAMMA1002268"
/tissue type="Mammary gland"
/clone_lib="MAMMA1"
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/db_xref="GI:10433791"
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Web site: http://www.nisc.nih.gov/
Neb site: http://www.nisc.nih.gov/
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogf, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
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HSRPCDARLGSTDKELKAGAAATGSAPTAPGTPWQREPRVEWMDPAGGPRGVLPRPCR
VLYLINPRGGKGKALQLFRSHVQPLLABABISFLAMTERRHARELVRSEBLGKWDA
VLVWSGDGLWHEWYGKGEMERPWERTALGFCSLPAGSGNALAASILHYAGYSQVTNE
DLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGF1ADVDLESEKYRRLGEM
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WYVPDEDFYLJJLALHSHLGSEMFAAPMGRCAAGVMILFYVRAGVSRANLIRLFLAM
BKGRHMEYECPYLVYPVVAFRLEFKDGKGVFAVDGELMVSEAVQGQVHPNYFMVSG
CVEPPPSWKPQQMPPPEEPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 64 Row: k Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361087. Location/Qualifiers
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Strausberg, R. Direct Submission Submitted (07-MAY-2002) National Institutes of Health, Mammalian Submitted (07-MAY-2002) National Institutes Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
CDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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Pred. No. 6.6e-211;
0; Mismatches 9; Indels 0;
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/tissue type="Blood, adult leukocytes"
/clone=lib="NIH MGC_118"
/lab host="DH108"
/note="Vector: pCMV-SPORT6"
                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/gene="SPHK1"
/codon_start=1
/product="sphingosine kinase 1"
/protein_id="AAH30553.1"
/db_xref="GI:22539643"
/db_xref="LocusID:8877"
/db_xref="MIM:603730"
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/organism="Homo sapiens"
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/db_xref="LocusID:8877"
/db_xref="MIM:603730"
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/db_xref="taxon:9606"
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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 15393 07-FEB-2001; Research Association for Biotechnology (JP)
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JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
KEIICHI NAGAI,TETSUJI OTSUKI
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Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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96.8%; Score 1167; DB 6;
Best Local Similarity 99.2%; Pred. No. 1.4e-210;
Matches 1173; Conservative 0; Mismatches 10;
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                    BD158407.1 GI:27864165
JP 2002191363-A/13250.
Homo sapiens (human)
Homo sapiens
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TGCCCGACGAGGACTTTGTGCTAGTCCTGGCACTGCTGCACTCGGACCTGGGCAGTGAGA	1027	AK023393  1772 bp mRNA linear PRI 30-JAN-2004 similar to Mus musculus sphingosine kinase (SPHKIa) mcNa.  AK023393  AK023393 AK023393 GI:10435311  Oligo capping; fis (full insert sequence).  Homo sapiens (human)  Memmalia; Butheria; Craniata; Vertebrata; Buteleostomi; Maxmares, A. Hayashi, K., Saco, H., Nagai, K., Kimura, T., Irie, R., Maxamateu, A., Hayashi, K., Saco, H., Nagai, K., Kimura, T., Irie, R., Nagai, K., Yamanoto, J., Salibahara, T., Tanaka, T., Tanaka, T., Shibahari, Y., Namura, Y., Shibahari, K., Murakami, K., Yauda, T., Isono, Y., Nagatsuma, M., Shirkawa, E., Ohura, Y., Abe, K., Kaku, Y., Kodaira, H., Kondo, H., Shikawa, E., Omura, Y., Abe, K., Kamihara, K., Sato, H., Katsuta, N., Sato, H., Kanahara, K., Katsuta, N., Sato, K., Katsuta, N., Sato, K., Tanaka, M., Sato, K., Tanaka, M., Watanabi, M., Yamazaki, M., Ninomiya, K., Tanai, H., Warahanabi, M., Watanabe, M., Watanabe, M., Watanabe, M., Watanabe, M., Watanabe, M.,	Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watchaabe,S., Yosida,M., Hotuta,T., Kusano,J., Kamehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Acteuka,S., Yoshikwa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yomojama,M., Fujino,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujino,Y., Makajima,Y., Mizuno,M., Shigeta,K., Senba,T., Maksimi,T., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Nakaina,Y., Matanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nasaki,M., Togashi,T., Makai,M., Yada,T., Nawamura,Y., Ohara,O., Isogai,T. and Sugano,S. Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S. Omplete sequencing and characterization of 21,243 full-length
88888888	8 8 8 8 8	RESULT 13 AK023393 LOCUS DECINITION ACCESSION VERSION VERSION CEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE
1. 1772	Query Match   96.8%;   Score 1167;   DB 6;   Length 1772;	127 AGCTCTTCCGGAGTCACGTGCAGCCCTTTTGGCTGAGATTCTCCTTCACGCTGA 186 444 AGCTCTTCCGGAGTCACGTGCAGCCCTTTTGGCTGAAATCTCCTTCACGCTGA 503 187 TGCTCACTGGGAGGCCGGAACCCGCGGGAGCTGGAGCTGGAGCTGGCGCTG 503 187 TGCTCACTGAGCGGGGAACCACGCGGGAGCTGGTGCGGCGGCT 246 504 TGCTCACTGGGGAACCACGCGGGGAGCTGGTGCGGTGAACGGCTG 563 247 GGGACGCTCTGGTGGTCATGTCTGGAACGGGGTGAACGGGCTGA 623 307 TGGAGCGCTCTGGTGGTCATGTCTGGAACGGGCTGATGCACGGGTGAACGGCTCA 623 307 TGGAGCGCTCATGGTGTCTGGAACGGGCTGATGCACGAGGTGAACGGGCTC 306 564 GGCACGCTCTGGTGGTCATGTCTGGAACGGGCTGATGCACGGGTCAACGGCTCAGAGGTCAACGGCTCAGAGCTCAGAGCCTCAGAGCCTGACTGA	487 TGCTGTCTCTGCACACGGCTTCGGGGCTTCTTCTTCTGTGCTCAGCCTGGG 546

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linear PRI 03-OCT-2003 (cDNA clone MGC:15041
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TGGAGCGGCCTGACTGGGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCT
                            CTGGCAACGCGCTGGCAGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATG
                                                                                                                                                                                                                     AAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGCCGGCTGCTGTCACCCATGAACC
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AEISFTLMLTERRNHARELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQ
KPLCSLPAGSGNALAASLNHYAGYBCDTTNCTLLLCRRLLSPWILSHHTASG
IRLESYLSLAMGFTADVDLESEKYRRLGEMRFTLGTFLRLAALRTYGRLAYLPVGRY
GSKTPASPVVQQGPVDAHLVPLEEPVPSHWTVVPDBDFVLVLALHSHLGSBMFAAP
MGRCAAGVMHLFYYAGVSRAMLLRLFLAMBKGRHMEYECPYLVYVPVVAFRLEFKDG
KGVFAVDGELMVSEAVQGQVHPNYFWWVSGCVEPPFSWKPQQMPPFEEPL"
                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission

Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'-& 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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                                                                                                             Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wasatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakawi, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, R., Ishii, S., Kawai, K., Masahari, K., Masahari, K., Masahari, K., Masahari, K., Masahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. NEDO, human cDNA sequencing project
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/clone_lib="OVARC1"
/note="cloning vector: pME188FL3"
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/db_xref="GI:10435312"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                           (1), 40-45 (2004)
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Matches 1173; Conservative
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/gene="SPHKI"
/note="LCB5; Region: Sphingosine kinase and enzy
related to eukaryotic diacylglycerol kinase [Lig
metabolism / General function prediction only]"
/db_xref="CDD:COG1597"
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Pred. No. 2.7e-210;
0; Mismatches 11; Indels
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Best Local Similarity 99.1%;
Matches 1172; Conservative
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       Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausberg, R.L., Feingold, E.A., Grouse, L.H., Schamen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Heieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunaranne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Hellon, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Generan, M.C., Schein, J.E., Jones, S.J. and Marra, M.A. Genen, L.D. Human, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 24 Row: n Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361087.
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/translation="MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Systems Biology
Nttp://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:14165485.
Contact: MGC help desk
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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'db_xref="GI:14165486"
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db_xref="MIM:603730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences
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note="synonym: SPHK"
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GSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAP
MGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDG
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M.B., Bornstein, R.J., Ushin, G.M., Hong, L.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skallaka, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
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Homo sapiens sphingosine kinase 1, mRNA (cDNA clone MG:22956
HMMGE:4871343), complete cds.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2133)
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                                                             AGGATGGGAAAGGTATGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGG
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNa Library Preparation: Rubin Laboratory
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov.Series: IRAL Plate: 34 Row: 1 Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361087.
Location/Qualifiers
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LVVMSGDGLMHEVVNGLMBRPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNB
DLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEM
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WTVVPDEDFYLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAM
EKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSG
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/product="sphingosine kinase 1"
/protein_id="AAH14439.1"
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/db_xref="MIM.603130"
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
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96.7%; Score 1165.4; DB 9;
Best Local Similarity 99.1%; Pred. No. 2.7e-210;
Matches 1172; Conservative 0; Mismatches 11;
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/db_xref="LocusID:8877"
/db_xref="MIM:603730"
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Search completed: June 17, 2005, 05:29:38 Job time : 5410 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

- nucleic search, using sw model OM nucleic June 17, 2005, 02:28:43; Search time 728 Seconds (without alignments) 9798.473 Million cell updates/sec Run on:

US-10-642-289-1 1205 Title: Perfect score: Sequence:

1 gaattcggcacgaggagccg.....gatctagagtcgacctgcag 1205 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched: 8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* N Geneseq\_16Dec04:\* 1: geneseqn1980s:\* 2: geneseqn1990s:\*

geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2004as:\* geneseqn2004bs:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result	9700	Query	Query Match Length DB	ä	1	Description
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			}		
-	1205	100.0	1205	2	AAC84161	Aac84161 Human sph
8	1173	97.3	1173	9	ABL59532	Abl59532 Human sph
ı en	1168.6	97.0	1573	m	AAA75676	Aaa75676 DNA encod
4	1168.6	97.0	1719	Ŋ	AAD04477	Aad04477 Human sph
ď	1168.6	97.0	1821	4	AAH15652	Aah15652 Human cDN
œ	1168.6	97.0	2137	10	ADD29776	Add29776 Human tum
7	1168.2	96.9	1799	10	ADE38364	Ade38364 Human pro
· 60	1167	96.8	1772	4	AAH16415	Aah16415 Human cDN
σ	1162.6	96.5	1783	12	AD017904	Adq17904 Human sof
9	1149.4	95.4	1533	7	AAV84490	Aav84490 Human sec
<u>)</u> :	1149.4	95.4	1533	4	ABA83273	Aba83273 Human sec
12	1149.4	95.4	1533	σ	ACH04774	Ach04774 Novel hum
13	1149.4	95.4	1533	0	ACD44584	Acd44584 Human cDN
14	1147	95.2	1155	9	ABK90198	Abk90198 cDNA enco
15	1145.8	95.1	1438	4	AA159336	Aai59336 Human pol
16	1143.8	94.9	1447	m	AAA50508	Aaa50508 Human sph
17	1142.4	94.8	1152	6	ACF35857	Acf35857 Human sph
18	1141.4	94.7	1600	s	AAD14424	Aad14424 Human sph
c 19	1140.4	94.6	1562	9	ABL90618	Abl90618 Human pol
20	1140.4	94.6	1869	12	ADJ74940	Adj74940 Marker ge

Novel sphingosine kinase protein and nucleic acid molecules for diagnosis, prophylaxis and treatment of rheumatoid arthritis, asthma, atherosclerosis, inflammation, meningitis, multiple sclerosis and septic shock.

Ado22416 Human sph Ado22418 Human sph Add22519 Human sof Aai61122 Human pol Aai61122 Human pol Aad14425 Mouse con Abx90200 CDNA enco			Add8/011 Human Cum Abx71285 Human sig Aas14816 Mouse CDN Aad04478 Conserved Aah10443 Human CDN Adq49460 Novel Can
12 ADO22416 12 ADO22418 12 ADQ22519 4 AAI61122 5 AAD14425 6 ABK90200	AAZ4/16/ AAZ47168 2 ADJ75835 0 ABZ81300 AAH07214 ABK90199	AAS14817 ABL59533 0 AD885298 0 AD838416 2 ADQ15181 AAS85331 2 ADQ83707	3 ADQ87011 3 ABX71285 AAX114816 AAD04478 AAH10443 3 ADQ49460
	1815 3 1559 3 1559 1 1146 1 675 4		2682 1 2875 5 2698 5 240 5 587 4 549 1
994.6 925.5 75.6 63.19	62.9 62.8 62.8 22.4 21.6	22222222222222222222222222222222222222	21.4 20.3 20.3 19.9 18.5
1140.4 1140 11115.2 910.8 770.4	757.6 756.6 756.6 752 272	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	258 245.2 240 235 227.8
222 222 222 222 232 242 254	27 28 31 31 31		C 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

Sphingosine kinase; antiarthritic; antiasthmatic; antiarteriosclerotic; antiinflammatory; neuroprotective; antibacterial; immunosuppressive; Gamble JR; Pitson SM, Wattenberg BW, Xia P, D'andrea RJ, /product= "sphingosine kinase" Human sphingosine kinase encoding cDNA. (JOHJ ) JOHNSON & JOHNSON RES PTY LTD. Location/Qualifiers 33. 1187 /\*tag= a AAC84161 standard; cDNA; 1205 BP. 99AU-00000339. 99AU-00001504. 12-MAY-2000; 2000WO-AU000457. 19-MAR-2001 (first entry) WPI; 2001-016227/02. P-PSDB; AAB48007. WO200070028-A1. 13-MAY-1999; 08-JUL-1999; Homo sapiens human; ss.. 23-NOV-2000. Vadas MA; AAC84161; Key RESULT 1 AAC84161  a

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GTGAGATGTTTGCTGCACCCATGGGCCGCTGTGCAGCTGGCGTCATGCATCTTTTACA
                                                                                    TGCGGCCGGGAGTGTCTCGTGCCATGCTGCTGCCCTCTTCCTGGCCATGGAGGGCA
                                                                                                                                                                                                                AGCCCAAGGATGGGAAAGGTATGTTTGCAGTGGAATGGGAATTGATGGTTAGCGAGGCCG
                                                                                                                                                                                                                                                                                                                           TGCAGGGCCAGGTGCACCCAAACTACTTCTGGATGGTCAGCGGGTTGCGTGGAGCCCCCGC
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                                                                                                                                      GGCATATGGAGTATGAATGCCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCTTGG
                                                                                                                                                            GGCATATGGAGTATGAATGCCCCTACTTGGTATATGTGCCCGTGGTCGCTTCCGCTTTCG
                                                                                                                                                                                                                                             TGCAGGGCCAGGTGCACCCCAAACTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCGC
                                                                                                                                                                                                                                                                                                                                                                     CCAGCTGGAAGCCCCAGCAGATGCCACCGCCAGAAGAGCCCTTATGATCTAGAGTCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, sphingosine kinase, SphK1, enzyme; chromosome 17q25.2; gene, tumour; lipid associated gene; lipid metabolism; lipid synthesis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying tumor characteristics in a tissue sample taken from a patient, involves determining the copy number or expression level genes associated with lipid metabolism, synthesis or action.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human sphingosine kinase (SphK1) cDNA SEQ ID NO:32
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                                  This cDNA encodes a human sphingosine kinase (SK) protein. The human SK protein, encoding nucleic acids and modulators are useful for modulating expression, functional activity or cellular functional activity of sphingosine kinase in a subject and also for treating a mammal by modulating the activity of SK. Diseases treated by regulating SK cellulan activity include rheumatoid arthritis, asthma, atherosclerosis,
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ive 0; Mismatches 0;
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the array comprises nucleic acid polymers which are specific for less than 100 genes other than the selected genes. The method is useful for determining tumour characteristics in a tissue sample taken from a patient. The present sequence represents a human lipid-associated generalated cDNA sequence, which is used in the exemplification of the
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                                                                                                                                                                 Sequence 1173 BP; 188 A; 349 C; 390 G; 246 T; 0 U; 0 Other;
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100.0%; Pred. No. 4.6e-259;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "regulator of intracellular phosphorylation"
                                                                                                                                                    HRIP; stroke; myeloma,
              AAAGGTATGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTG
GAATGCCCCTACTTGGTATATGTGCCCCGTGGTCGCCTTCCGCTTGGAGCCCCAAGGATGGG
                                                                                                                                        Human, intracellular phosphorylation regulator; HRIP; stroke; myelon neurological disorder; Parkinson's disease; demyelinating disease; meningitis; developmental disorder; neuromuscular disorder; cancer; maysthenia gravis; cell proliferative disorder; actinic keracosis arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis; autorimmune disorder; inflammatory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus; rheumatoid arthritis; microbial infection; trauma; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and
                                                                                                                                                                                                                                                                                                                                          DNA encoding a human regulator of intracellular phosphorylation
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antagonists of HRIP polypeptide. HRIP and its agonist or antagonist are useful for treating a disease or condition associated with decreased or increased expression of functional HRIP. Diseases treated or diagnosed include neurological disorders such as stroke, Parkinson's disease, dewyelinating diseases, bacterial and viral meningitis and other developmental disorders of the central nervous system, neuromuscular disorders, myasthenia gravis, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer including leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder, bone, bonne marrow, liver, lung, muscle, ovary, autoimmune/ inflammatory disorder such as Addison's disease, acquired immunodeficiency diseases, allergies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial
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                                                                                                                                                                                  Sequence 1573 BP; 274 A; 480 C; 514 G; 305 T; 0 U; 0 Other;
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Matches 1174; Conservative
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/note= "Translational initiator ATG is in a partial Kozak
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/*tag= a

/product= "Human sphingosine kinase type 1 (hsk1)"

/note= "CDS is specifically claimed in claim 2 and shown

as SEQ ID NO 2"

1675. .1681

/*tag= b
TGTTTGCTGCACCCATGGGCCGCTGTGCAGCTGGCGTCATGCTATTGTTCTACGTGCGGG
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                                                                                            TGTTTGCTGCACCCATGGGCCGCTGTGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGG
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TCACTCTGGGCACTTTCCTGCGTCTGGCCACCTTGCGCACTTACCGCGGCCGACTGGCTT
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899
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                                                                                                                                                                                                                                                                                                                 The present sequence is human sphingosine kinase type 1 (hsk1) cDNA. The hsk1 gene is located on chromosome 17q25.2. The sk1 converts the substrate sphingosine to sphingosine-1-phosphate (S1P). The sk1 gene and encoded polypeptide are applicable in screening drug candidates particularly inhibitors for preventing or treating disorders such as haemostasis, thrombosis, allergic reactions, proliferative diseases including cancer, haematopoietic disorders such as leukaemia, cardiovascular diseases such as stroke, atherosclerosis and coronary artery disease, dyslipidaemia, diabetes including type I and type II diabetes, autoimmune and inflammatory diseases such as multiple caclerosis, T helper-1 related diseases, chronic obstructive pulmonary disease, asthma, myocardial infarction, neurodegenerative disorders, natural wound healing processes and embryogenesis
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Pred. No. 5e-258;
0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1719 BP; 305 A; 529 C; 556 G; 329 T; 0 U; 0 Other;
                                                         Takacs L;
                                                         Melendez AJ,
                                                                                                                                                                                                                                                                                Claim 2; Fig 1; 91pp; English.
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Best Local Similarity 99.2%;
Matches 1174; Conservative
            (WARN ) WARNER LAMBERT CO
                                                         Gosink M,
                                                                                                    WPI; 2001-300510/31
P-PSDB; AAE00924.
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification, Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprisentary to the
complementary strand of a polymucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polymucleotide which comprises a some of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a forent complementary to a
complementary strand of a polymucleotide which comprises a feast 15 nucleotides and the combination of
complementary strand of a polymucleotide shich comprises at least 15 nucleotides and the compination of
complementary strand of a polymucleotide shich sequence, where the
complementary strand of sequence is selected from those defined in the
complementary the primer sets can be used in antisense therapy and in
gene therapy. The primer sets can useful for synthesising polymucleotides,
complementary the primers are useful for synthesising polymucleotides,
the full-length cDNAs. The primers are also useful for the
cundatoriarly full-length cDNAs. The primers allow obtaining of the full-length
connas and or diagnosis of the abnormality of the proteins encoded
AMH13613 to AMH1872 represent human amino acid sequences; and AMH13629 to AMH13629 represent
consignation of the abnormal condition of the
condition and sequences, and AMH13629 to AMH13632 represent
                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                        SEQ ID NO 13996; 2537pp + Sequence Listing; English.
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                                                                                                                                                                                                                        Claim 8;
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Sequence 1821 BP; 301 A; 569 C; 614 G; 337 T; 0 U; 0 Other;

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Score 1168.6; DB 4; Length 1821;
Pred. No. 5.1e-258;
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Query Match
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GCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAATGCGCT
               GCTTCATTGCTGATGTGGACCTAGAGAGAGAGAAGTATCGGCGCGTCTGGGGGGAGATGCGCT
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The invention relates to a novel method for diagnosing a cancer in a subject. the method comprises determing, in a sample from the subject, the level of at least one polypeptide, where a higher level of the subject, the level of at least one polypeptide in a subject free of cancer is indicative of cancer. The polypeptide in a subject free of cancer is indicative of cancer. The polypeptide is selected from any of the polypeptides listed in the polypeptides cancer is polypeptides of cancer. The polypeptide is selected from any of the polypeptides listed in the polypeptides. The method of the invention has cytostatic activity, and may have a use in gene therapy. The method is useful in identifying may have a use in gene therapy. The method is useful in identifying tissue origin, which may be used in numerous diagnostic and prognostic applications as well as cancer type-specific targets for therapeutic intervention. The compounds that modulate the activity of a tumour suppressor gene are useful in the treatment of cancer or as anti-cancer drugs. The present sequence represents a polynucleotide of the invention.
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level compared to that in a subject free of cancer is indicative of
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Pred. No. 5.2e-258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel method of treating a human subject having a tumourigenic disorder or angiogenic disorder, caused by aberrant gene expression or activity of an isolated protein, by administering a modulator. The modulator may have cytostatic, antithyroid, antidiabetic or ophthalmological activity. The method is useful for treating a subject having a tumourigenic or angiogenic disorder, in particular for treating cancer (for example breast cancer, colon cancer, lung cancer or prostatic cancer) and, for example, Grave's disease and diabetic retinopathy. The present sequence is a DNA sequence which encodes the novel isolated human protein 49863 of the invention.
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Pred. No. 6.38-258;
1; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1799 BP; 304 A; 565 C; 588 G; 339 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                     Lightcap ES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 25; 454pp; English.
                                                                                                                                                                                                                                                                                                 Hunter JJ, Macbeth KJ, Tsai F,
Williamson MW, Rudolph-Owen LA;
14-JUN-2002; 2002US-0382535F.
14-JUN-2002; 2002US-0388853F.
14-JUN-2002; 2002US-0388853F.
25-JUN-2002; 2002US-0389355P.
15-JUL-2002; 2002US-0395344P.
15-JUL-2002; 2002US-0395944P.
13-AUG-2002; 2002US-0403464F.
22-JUL-2002; 2002US-0405361P.
27-AUG-2002; 2002US-0405361P.
25-OCT-2002; 2002US-0405361P.
15-NOV-2002; 2002US-0425456F.
19-NOV-2002; 2002US-0425456F.
10-DEC-2002; 2002US-0425456F.
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99.28;
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Matches 1173; Conservative
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P-PSDB; ADE38365.
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CTGGCAACGCGCTGGCAGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATG
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                                                                                                                        AAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGCCGGCTGCTGTCACCCATGAACC
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                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
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                                                                                                                                                                                                                                                           Yamamoto J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; SEQ ID NO 15393; 2537pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                           Saito K, Y. Otsuki T;
                                                                                                                                                                                                                                                       Hayashi K, S.
A, Nagai K,
                                                                                                                                                                                                                                                                                           Wakamatsu
29-JUL-1999; 99JP-00248036.
27-ANG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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Sugiyama T, Wakama
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual dard a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic sack sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated bNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
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                                                                                                                                                                                                                                  Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                  Zlotnik A;
                                                                                                                                (PROT-) PROTEIN DESIGN LABS INC
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98.4%;
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                                                                  26-NOV-2003; 2003WO-US038193
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WO2004048938-A2
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The invention relates to nucleic acid sequences (AAV84411 to AAV84633)

cncoding human secreted proteins (AAV88534 to AAV88756). The secreted
cncoding human secreted proteins (AAV88534 to AAV88756). The secreted
cncoding human secreted proteins (AAV88534 to AAV88756). The secreted
CC protein gene sequences are deposited with the ATCC under deposit numbers
CC 209011, 209080, 209081, 209083, 209084, 209085, 209009, 209010,
CC 209011, 209080, 209081, 209083, 209084, 209085, 209511. Host
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynuclectide and anino acid sequences are useful for are
useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pethological conditions can be also diagnosed
CC protein or gene therapy. Pethological conditions can be also diagnosed
CC protein or gene therapy. Pethological conditions are described for each of the polynuclectides.
CC by protein or gene therapy. Pethological conditions are described for each of the polynuclectides.
CC specific uses are described for each of the polynuclectides.
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CC specific uses are described for each of the polynuclectides.
CC specific uses are described for each of the polynuclectides.
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, block
CC disorders, prostate diseases, lymphomas, inflammation, allergies,
CC schemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC schemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC rehymus, disperiive/endoxrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC describtor line for gene number and clone identification)
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                                                                                                                                                                                                                              Ferrie AM, Ruben SM, Rosen CA, Hu J;
Brewer LA, Moore PA, Shi Y, Florence C;
Mi J, Fan P, Wei Y, Fischer CL, Soppet DR;
H, Yu G, Feng P, Dillon PJ, Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 GGGACGCTCTGGTGGTCATGTCTGGAGACGGCTGATGCACGAGGTGGTGAACGGGC-TC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1533 BP; 272 A; 454 C; 495 G; 302 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 343; 772pp; English
97US-0057777P.
97US-0057778P.
97US-0070923P.
                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                              Young P, Greene JM, I
Olsen HS, Ebner R, B:
Florence K, Lafleur DV
Li Y, Zeng Z, Kyaw H,
Carter KC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-059865/05.
P-PSDB; AAW88613.
        05-SEP-1997;
                                            05-SEP-1997;
18-DEC-1997;
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cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotective; noticopic; anticonvulsant; antialzheimers; vulnerary; antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficioncy virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis; Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder; neurological disorder; Huntington's chorea; Alzheimer's disease; parkinson's disease; chromosome 17; ss.

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                                                      TCTGGCAACGCGCTGGCAGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAAT
                                                                                 TCTGGCAACGCSCTGGCAGCTTCCTTRAACCATTATGCTGGCTATRAGCAGGTCACCAAT
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disease

Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's

and diabetic retinopathy.

WPI; 2001-625724/72. P-PSDB; ABB50380.

bner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA; , Soppet DR, Young PE, Shi Y, Florence KA, Wei Y; C, Hu J, Li Y, Kyaw, Fischer CL, Ferrie AM, Fan P; Endress GA, Dillon PU, Carter KC, Brewer LA, Yu G, Zeng Z;

24-FEB-2000; 2000US-0184836P. 29-MAR-2000; 2000US-0193170P. 21-FEB-2001; 2001WO-US005614.

WO200162891-A2. Homo sapiens.

30-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC

Ebner R,

Florence C,

Ruben SM

Greene JM;

Feng P,

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proteins (I) and polynucleotide (II) sequences. (I) and (II) have various activities based on the tissues and cells the genes are expressed in. Example of these activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; immunostimulant; anti-angiogenic; obthialmological; immunosuppressive; antiinflammatory; immunostimulant; anti-angiogenic; opthialmological; or neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular; antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used in the prevention, diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and caucher's diseases), cardiovascular diseases (e.g. Schintar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), anglogenic disorders (e.g. conceal graft neovascularisation and diabetic cretinopathy, neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's diseases), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to ABA83193 and ABB83193 and ABB83193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Η;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 965; 1533pp; English.
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Human, secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antiinflammatory; immunostimulant;

Human secreted protein gene 80 SEQ ID NO:90.

(first entry)

07-FEB-2002

RESULT 11
ABA83273
XX
AC ABA83
XX
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DT 07-FF
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KW Humar
KW Humar
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ABA83273

ABA83273 standard; cDNA; 1533 BP.

RESULT 12 ACH04774

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                                                                                                    CIGCTGTCTCTGCACACGGCTTCGGGGCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGG
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          GGGACGCTCTGGTGATGTCTGGAGACGGCTGATGCACGAGGTGGAACGGGC-TC
                                                                                                                                   ATGGAGCGGCCTGACTGGGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGC
                                                                                                                                                TCTGGCAACGCGCTGGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAAT
                                                                                                                                                                                            GAAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGCCTGCTGTCACCCATGAAC
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AGCTCTTCCGGAGTCACGTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGA
                                           TGCTCACTGAGCGGCGGAACCACGCGGGGGGGCTGGTGCGGTCGGAGGAGCTGGGCCGCT
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Human; ss; gene therapy; autoimmune disorder; multiple sclerosis; cancer; systemic lupus erythematosus; haematopoietic cell disorder; allergy; agammaglobulinaemia; ataxia telangiectasia; blood coagulation disorder; afibrinogenaemia; thrombocytopenia; graft-versus-host disease; arthritis; inflammatory condition; ischaemia-reperfusion injury; infectious disease; hyperproliferative disorder; purpura; viral infection; regeneration; bacterial infection; ulcer; Alzheimer's disease; gene.
                                                      Novel human secreted protein #80 cDNA
BP
                                                                                                                                                                                                                         97US-0048875P.
97US-0048876P.
97US-0048817P.
97US-0048881P.
97US-0048881P.
97US-0048881P.
97US-0048884P.
97US-0048884P.
97US-0048884P.
97US-0048894P.
97US-0048899P.
97US-0048899P.
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97US-0048899P.
97US-004899P.
97US-004897P.
97US-005762P.
97US-005763P.
97US-005763P.
CDNA; 1533
                                                                                                                                                                                                         2001US-00004860
                                    entry)
                                    (first
ACH04774 standard;
                                                                                                                                                                     US2003065160-A1
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05-SEP-1997;
05-SEP-1997;
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                                                                                                                                                   Homo sapiens.
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
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                  ACH04774;
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Sequence 1533 BP; 272 A; 454 C; 495 G; 302 T; 0 U; 10 Other;
                                                                                                                                                     97US-0057776P.
97US-0057777P.
97US-0057778P.
97US-0070923P.
     97US-0057647P.
97US-0057648P.
97US-0057649P.
97US-0057650P.
97US-0057651P.
97US-0057651P.
                                                          97US-0057666P.
97US-0057667P.
97US-0057668P.
                                                                                     97US-0057761P.
97US-0057762P.
97US-0057763P.
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97US-0057765P.
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97US-0057771P.
97US-0057774P.
97US-0057775P.
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05-SEP-1997;
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18-DEC-1997;
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DR;
                                      Ruben SM, Rosen CA, Hu J;
Moore PA, Shi Y, Florence C;
Fan P, Wei Y, Fischer CL, Soppet
Feng P, Dillon PJ, Endress GA;
                                      Greene JM, Ferrie AM,
Ebner R, Brewer LA,
K, Lafleur DW, Ni J,
(HUMA-) HUMAN GENOME SCI INC
                                      Young P, Greene JM, Fer
Olsen HS, Ebner R, Brew
Florence K, Lafleur DW,
Li Y, Zeng Z, Kyaw H,
Carter KC;
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New isolated protein, useful for preparing a composition for diagnosing or treating cancer, inflammatory, immune or infectious diseases.

Example 1; SEQ ID NO 90; 172pp; English.

useful for preparing a composition for diagnosing or treating autoimmune disorders e.g. multiple sclerosis and systemic lupus erythematosus; haematopoietic cell disorders e.g. agammaglobulineemia and ataxia telangiectasia; blood coagulation disorders e.g. afibrinogenaemia and thrombocytopenia; allergy; graft-versus-host disease; inflammatory conditions e.g. ischaemia-reperfusion injury and arthritis; hyperproliferative disorders e.g. cancer and purpura; infectious disease e.g. viral infection and bacterial infection. The polymucleotide or protein can be used to regenerate damaged tissue e.g. ulcers and Alzheimer's disease. The srequence represents a novel human secreted protein cDNA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at The invention relates to an isolated HEMAE80 protein. The protein is segdata.uspto.gov/seguence.html?DocID=20030065160

GGCAGCGGGAGCCGCGGGTCGAGGTTATGGATCCAGCGGCGGCCCCCCGGGGCGCGCTCC 106 99 GGCACGAGGAGCCGCGGGTCGAGGTTATGGATCCAGCGGCGGCGCCCCCCGGGGCGTGCTCC 95.4%; Score 1149.4; DB 9; Length 1533; 98.3%; Pred. No. 1.2e-253; ive 6; Mismatches 13; Indels 1; Best Local Similarity 98.3 Matches 1164; Conservative 7 Query Match

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1007 AIGGAGTATGAATGCCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCC 1066 GGCCAGGTGCACCCCAAACTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGC 1145 ATGGAGTATGAATGCCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCC 1025 AAGGATGGGAAAGGTATGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAG 1085 305 166 ATGGAGCGGCCTGACTGGGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGC 406 425 545 286 ATGGAGCGCCTGACTGGGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGC 365 466 485 gaagaccrccrgaccaacrgcacgcrarrgcrgrgccgccggcrgcrgrcacccargaac 526 CTGCTGTCTCTGCACACGGCTTCGGGGCTGCGCCTCTTCTCTCTGTGCTCAGCCTGGCCTGG 586 605 TTCACTCTGGGCACTTTCCTGCGTCTGGCAGCCTTGCGCACTTACCGCGGCCGACTGGCT 665 rrcacrcrissicacertriceriscererissicas de consecuencia de conse 725 994 785 826 845 886 ATGTTTGCTGCACCCATGGGCCGCTGTGCAGCTGGCGTCATGCATCTGTTCTACGTGCGG 905 TCTGGCAACGCSCTGGCAGCTTCCTTRAACCATTATGCTGGCTATRAGCAGGTCACCAAT CGCGGCCCTGCCGCGTGCTGCTGCTGCTGCTGCCCGCGCGCGCGCGCAAGGCCAAGGCCTTGC CGCGGCCCTGCCGGTGNCTGGTGCTGCTGAACCCGCGCGGCGGCGAAGGGCAAAGGCCTTGC TGCTCACTGAGCGGCGGAACCACGCGCGGGAGCTGCTGCGGTCGGAGGAGCTGGGCCGCT TGCTCACTGAGGGGGGAACCACGCGGGGGARCTGGTGCGGTCGGAGGAGGAGCTGGGCCGCT GGGACGCTCTGGTGGTCATGTCTGGAGACGGGCTGATGCACGAGGTGGTGAACGGGC-TC GGRACGCTCTGGTGGTCATGTYTGGAGACGGCTGATGCACGAGGTGGTGAACGGCCTTC GAAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGCCGGCTGCTGTCACCATGAAC TACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAG TACCTCCCTGTAGGAAGAGGGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAG GGCCCGGTAGATGCACCTTGTGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTG GGCCCGGTAGATGCACACTTGTGCCACTGGAGGAGGAGCAGTGCCCTCTCACTGGACAGTG GIGCCCGACGACGACTITIGIGETAGTCCTGGCACTGCTCCACTCCCTGGCAGTGAG ATGTTTGCTGCACCCATGGGCCGCTGTGCAGCTGGCGTCATGCATCTGTTCTACGTGCGG TCTGGCAACGCGCTGGCAGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAAT CTGCTGTCTCTGCACACACGGCTTCGGGGCTGCCCTCTTCTCTGTGCTCAGCCTGGCCTGG GGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGC GTGCCCGACGAGGACTTTGTGCTAGTCCTGGCACTGCTGCACTCGCACCTGGGCAGTGAG 1067 227 306 347 407 647 999 846 887 947 1026 107 127 167 187 247 287 366 426 467 486 527 546 587 909 707 726 167 786 827 906 996

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Sequence 1533 BP; 272 A; 454 C; 495 G; 302 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Human; ss; gene; secreted protein; precerebellin-like protein; neurodegenerative disorder; behavioural disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia; mania; dementia, paranoia; psychosis; autism; immune disorder; infection; inflammation; allergy; liver disorder; hepatoblastom; jaundice; hepatitis; immunological disorder; hepatoblastoma; jaundice; sepsis; acne; psoriasis; cancer.
1146 TGGAAGCCCCAGCAGATGCCACCGCCAGAAGAGCCCTTATGATC 1189
        Human cDNA from novel secreted protein gene 80.
                                                     ACD44584 standard; cDNA; 1533 BP.
                                                                                                                                                                                                                                             97US-0048876P.
97US-0048878P.
97US-0048881P.
97US-0048881P.
97US-0048881P.
97US-0048882P.
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                                                                                   (first entry)
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06-JUN-1997;
06-JUN-1997;
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06 - JUN - 1997
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06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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                                                                    ACD44584;
                                      RESULT 1
ACD44584
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The invention relates to an isolated protein comprising amino acid
residues 33-205 or 1-205 of a novel human secreted protein appearing as
residues 33-205 or 1-205 of a novel human secreted protein appearing as
apposed 23.

ABO26252. The protein is encoded by one of 238 disclosed cDNA sequences
concoling 238 secreted proteins. ABO26252 is a precerebellin-like protein.

Also included are a composition comprising the protein and a carrier and
an isolated protein produced by expressing the protein cited above by a
cell, and recovering the protein. The protein cited above by a
cell, and recovering the protein. The protein cited above by a
contracting neurodegenerative and behavioural disorders (e.g. Alzheimer's
disease, Parkinson's disease, Huntington's disease, schizophrenia, mania,
dementia, paramoia, psychoses or autism), immune disorders (e.g. Alzheimer's
infection, inflammation, allergy), liver disorders (e.g. hepatolastoma,
jaundice, hepatitis), immunological disorders (e.g. AlDS, leukaemia,
c'aundice, hepatitis), the 228 diselosed colNNs encoding a novel secreted
c'archimed specification, but was obtained in electronic format directly
c'archimed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Ruben SM, Rosen CA, Hu J;
Moore PA, Shi Y, Florence C;
Fan P, Wei Y, Fischer CL, So
Feng P, Dillon DJ, Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 90; 156pp; English.
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DW, Ni J,
H, Yu G, E
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9705-0057651P-
9705-0057651P-
9705-0057662P-
9705-0057668P-
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9705-0057761P-
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Olsen HS, Ebner R, Br
Florence K, Lafleur DW
Li Y, Zeng Z, Kyaw H,
Carter KC;
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95.4%; Score 1149.4; DB 9; Length 1533;

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The present invention relates to a new method of inducing blood vessel formation in an animal. The method of the invention involves administering sphingosine kinase to the animal. The method is useful for inducing blood vessel formation in an animal, or preventing or treating congestive heart failure, myocardial ischaemia, ischaemia-reperfusion injury and peripheral arterial diseases in an animal, e.g. mammal (such sprimate including human). The invention is also useful for treating injury and disorders selected from coronary artery disease, peripheral vascular disease, wound healing and fracture repair, reconstructive surgery, transplantation such as islet transplants, tendon repair/sports injury, healing of ulcers, thromboangitis obliterans (Buerger's disease), periodontal tissue regeneration and radiocherapy-induced oesophagitis. The present nucleic acid sequence encodes the human sphingosine kinase I (SPHKI) protein as described in the invention
1067 AAGGATGGGAAAGGTGTGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAG 1126
                                                                                                                                                                                                                                                                                                                                        Human; sphingosine Kinase 1; SPHKI; blood vessel formation; primate; congestive heart failure; myocardial ischaemia; wound healing; ischaemia-reperfusion injury; peripheral arterial disease; angiogenesis; coronary artery disease; peripheral vascular disease; fracture repair; reconstructive surgery; transplantation; islet transplant; tendon repair; sports injury; ulcer; thromboangitis obliterans; Buerger's disease; gene; periodontal tissue regeneration; radiotherapy-induced oesophagitis; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing blood vessel formation, or preventing/treating congestive heart failure, ischemia-reperfusion injury, myocardial ischemia and peripheral arterial diseases in animal, by administering sphingosine kinase.
                                 GGCCAGGTGCACCCAAACTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGC
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/product= "Human sphingosine kinase 1 (SPHK1)"
                                                                                                                  TGGAAGCCCCAGCAGATGCCACCGCCAGAAGAGCCCTTATGACC 1230
                                                                                                TGGAAGCCCCAGCAGATGCCACCGCCAGAAGAGCCCCTTATGATC 1189
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NOVARTIS-ERFINDUNGEN VERW GES
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                               ATGGTCAGCGGGTTGCGTGGAGCCCCCGGCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroals; Shy-brager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                     GATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGCCCAGGTGCACCCCAAACTACTTCTGG
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25-APR-2000; 2000US-00552317.
20-UUN-2000; 2000US-00598042.
19-UUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-006631936.
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2000US-00488725.
2000US-00552317.
2000US-00598042.
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C; 382 G; 239 T; 0 U; 0 Other;
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                                       Score 1147; DB 6;
Pred. No. 4.2e-253;
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Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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Pred. No. 8.2e-253;
0; Mismatches 7; Indels 0;
                                                                                                                      Sequence 1438 BP; 251 A; 428 C; 463 G; 296 T; 0 U; 0 Other;
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TATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCCAAGGATGGGAAAGGTATGTTTGCAGTG
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 9b est1:\* 9b est2:\* 9b est2:\* 9b est4:\* 9b est5:\* 9b est5:\* 9b gss1:\* EST:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description				BI860351 603387479		BX401290 BX401290		-	w					BG678689 602624488	BM006005 603613736	AV694791 AV694791	σ	80		BG026631 602293762	BQ675531 AGENCOURT	BP267514 BP267514		60327	CV028128 6543 Full
SUMMARIES	<b>Q</b>		BM808698	BM810136	BI860351	AY415128	BX401290	BG680521	BQ647377	BM916526	BX362837	BX363407	BX398860	CV027223	BG678689	BM006005	AV694791	AY415129	BX362838	BE891653	BG026631	BQ675531	BP267514	CN156333	BI648186	CV028128
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de	Query Match		72.1	69.7	6.99	64.1	61.4	60.2	59.4	58.8	58.1	57.6	54.6	51.9	51.7	51.0	50.3	49.9	49.3	49.3	49.3	48.5	47.2	47.1	43.7	43.2
	Score		868.6	839.4	906.6	773	739.8	725.2	715.2	708.8	699.8	694.6	657.4	625.6	622.6	614.4	606.4	601.6	594.6	593.8	593.6	584.6	569.2	567.6	526.2	520
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ORIGIN

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BX398861	BC011432	AY415130	AK028667	BX363408	CD518980	BI415545	BM559257	AI769914	BU158134	BE274434	BM557357	BE740866	CA307119	CK969307	BG280830	BE275818	CD366097	BU626812	BU630558	AW916618
BX398861	BC011432	AY415130	AK028667	BX363408	CD518980	BI415545	BM559257	AI769914	BU158134	BE274434	BM557357	BE740866	CA307119	CK969307	BG280830	BE275818	CD366097	BU626812	BU630558	AW916618
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/tissue type="amelanotic melanoma, cell line"
/lab_host="nBH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site 1: Xho1; Site 2:
ECRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoR1/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                          EST 05-MAR-2002
                                                                                            ACENCOURT 6579661 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5470089 BM810136
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabe.remail.nih.gov
Tissue Procurement: DCTD/DrP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLCMA.976 row: f column: 10
High quality sequence stop: 623.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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AUTHORS
TITLE
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                                                                               CCTTCACGCTGATGCTCACTGAGCGGCGGGAACCACGCGCGGGGAGCTGCGGTCCGGAGG
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                                          Gaps
                                        12;
  Length 1054;
                                        Indels
  4,
                                          44;
                       6.1e-194;
  DB
Score 868.6; D
Pred. No. 6.1e-
0; Mismatches
72.1%;
94.5%;
Query Match
Best Local Similarity 94.5
Matches 967; Conservative
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/ MOJ_LYPE="MRXN" | MOJ_LYPE="MRXN" | MOJ_LYPE="MRXN" | MOJ_LYPE="MRXN" | MOS xref="taxon:9606" | Alone="LMAGE:5396178" | Alone="LMAGE:5396178" | Alone="LMAGE:5396178" | Alone="DHLOB (phage-resistant)" | Alone="DHLOB (phage-resistant)" | Alone="DHLOB (phage-resistant)" | Alone="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI; Anore="Grgan: breast; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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96.8%; Pred. No. 2.5e-179;
ive 0; Mismatches 24;
                                    organism="Homo sapiens"
Location/Qualifiers
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866; Conser
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1 (bases 1 to 82)

NIH-MGC http://mgc.nci.nih.gov/.

Sanional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapberremail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M. AG.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M. A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12009 row: n column: 19

High quality sequence stop: 878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI860351 892 bp mRNA linear EST 10-OCT-2001
603387479F1 NIH_MGC_87 Homo sapiens CDNA clone IMAGE:5396178 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTATATGTG-CCCGTGGTCGCCTTC 1013
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX401290 Homo sapiens HELA CELLS COT 25-NORWALIZED Homo sapiens COT 25-NORWALIZED Homo sapiens CDNA clone CSODK011XD19 3-PRIME, mRNA sequence.

EX401290
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1102)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30626413.
Contact: Genoscope
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/db_xref="taxon:9606"
/clone="CSODKOllYD19"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/clone lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
                           CCCCGTTGTGGTCCAGCAGGCCCGGTAGATGCACACTTGTGCCACTGGAGGGGGCCAGT
                                                                                                               GCCCTCTCACTGGACACAGTGGCCCGACGAGGACTTTGTGCTAGTCCTGGCACTGCTGCA
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241 CTACCGCGGCCGACTGGCCTACCTCTAGGAAGAGTGGGTTCCAAGACACTGCCTC 300
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Clark, A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Fodd,M.A., Tanenbaum,D.M., Civello,D.R., Lu.F., Murphy,B., Ferriera,S., Wanoy,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
2 (bases 1 to 781)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                              TGCGTGGAGCCCCCCCCCAGCTGGAAGCCCCCAGCAGATGCCACCCCCCAGAAGAGC 1179
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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genomic survey sequence.
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62628344F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753187 S',
mRNA sequence.
BG680521
BG680521.1 GI:13911918
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  primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR I sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                       Query Match 61.4%; Score 739.8; DB 5; Best Local Similarity 98.3%; Pred. No. 1.4e-163; Matches 789; Conservative 1; Mismatches 8;
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Concert: Cor 785;

NH-MGC http://mgc.nci.nih.gov/.

Luckinal Institutes of Health, Mammalian Gene Collection (MGC)

Luckinal Institutes of Health, Mammalian Gene Collection (MGC)

Luckinal Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

Contact: Robert Straved by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLAM10612 row; g column: 12

High quality sequence stop: 783.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Skn4"
/note="Cogan: skin; Wector: pCMV-SPORT6; Site_l: NotI;
Site_2: Sol; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4753187"
sapiens (human)
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AGENCOURT_6641989 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5482958
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1100)

NHH-MGC http://mgc.nci.nih.gov/.

NAtional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
                                                           CCACTGCACGCTATTGCTGTGCCGCCGGCTGCTGTCACCCCATGAACCTGCTGTCTCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGENCOURT 8414975 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6272071
5., mRNA Sequence.
                                     TGGCCATGGAGAGGCCAGGCATATGGAGTATGAATGCCCCTACTTGGTATATGTGCCCG 1002
                                                                                                                 TGGTCGCCTTCCGC-TTGGAGCCCCAAGGATGGGAAAGGTATGTTTGCAGTGGATGGGGAA 1061
                                                                                                                                                                                          TTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGGATGGTCAGC 1121
                                                                                                                                                                                                                                                                      GGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCAGAAGAGCCC 1181
                                                           541 TGGCCATGGAGAAGGCCAGGCATATGGAGTATGAATGCCCCCTACTTGGTATATGTGCCC 600
                                                                                                                                     601 TGGTCGCCTTCCGCTTTGGAGCCCCAAGGATGGGAAAGGTGTTTTGCAGTGGATGGGGAA 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: Rhe I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCMA449 row: n column: 08
High quality sequence start: 6
High quality sequence stop: 668.
                                                                                                                                                                                                                                                                                             719 GGTTGCGTGGAGCCCCCG-CCAGCTGGAAGCCCCAGCAGATGCCACCG-CAGAAGAGAGCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Pred. No. 8.7e-158;
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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Best Local Similarity
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1 (bases 1 to 979)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
Unpublished (2001)
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/cell_line="HELA"
/clone lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODK004CH11NP1.
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Pred. No. 3.8e-154;
4; Mismatches 6;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK004YP21"
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Best Local Similarity 98.3
Matches 734; Conservative
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                                                CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2009 row: n column: 15
High quality sequence stop: 625.
Location/Qualifiers
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Pred. No. 2.9e-156;
0; Mismatches 80; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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/organism="Homo sapiens"
/mol type="maxA."
/db Zref="taxon:9606"
/db Zref="taxon:9606"
/dlone="GSDEXOLZYLL5"
/cell type="HELA CELLS COT 25-NORMALIZED"
/cell line="HELA"
/clone lib="HOMA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand CDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized."
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Location/Qualifiers
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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BX363407 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODK012YL15 3-PRIME, mRNA sequence.
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                                                                                                                                CCTGCGTCTGGCAGCCCTGCGCACCTACCCGCGGCCGACTGGCCTACCTCTGTAGGAAG
                                                                                                                                                                                                         AGTGGGTTCCAAGACACCTGCCCCCGTTGTGTCCAGCAGGGCCCGGTAGATGCACA
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GGCTTCGGGG-TGCGCCTCTTCTCTGTGCTCAGCCTGGGGCTTCATTGCTGATGT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 955)

1. (bases 1 to 955)

2. (contact: Gangeroe; C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization

1. Unpublished (2001)

2. num And 13, 2003 this sequence version replaced gi:30613804.

Contact: Gangeroepe - Centre National de Sequencage

2. rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecos V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                        EST 28-APR-2004
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                        O MRNA linear EST 28-APR-2000
COT 25-NORMALIZED Homo sapiens CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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llarity 96.0%; Pred. No. 3.8e-144;
Conservative 7; Mismatches 18;
                                                           clone CS0DI065YH09 3-PRIME, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                      995 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="mRNA"
|db_xref="taxon:9606"
|clone="CS0DI065YH09"
                                          BX398860 Homo sapiens PLACENTA
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                                                                                                                                sapiens (human)
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/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CV027223 633 bp mRNA linear EST 20-AUG-2004 5423 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC008040, mRNA sequence.
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
1 Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length CDNA as
                                                                                                                                                                                                1062
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487
                                                                                                                                  427
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 633)
                                                                                                486 IGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTATACGTGCCCG
                                                                                                                                                                                                TGGTCGCCTTCCGCTTGGAGCCCCAAGGATGGGAAAGGTATGTTTGCAGTGGATGGGGAAT
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/db_xref="taxon:9606"
/dbsue_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
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Insert Length: 633 Std Error: 18.00
Plate: 11059 row: 10 column: E
Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
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High quality sequence stop: 632
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827 CTCGCACCTGGG--CAGTGAGATGTTTGCTGCACCCATGGGCCGCTGTG---CAGCTGGC 881
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Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
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602624488F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4749573 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 793)
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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0; Mismatches 4;
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/lab host="DHIOB (TI phage-resistant)"
/clone_lib="NCI CGAP_StA4"
/note="Organ: skin, Vector: pCWV-SPORT6, Site_1: Not1;
/note="Organ: skin, Vector: pCWV-SPORT6, Site_1: Not1,
/note="I cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10602 row: p column: 22
High quality sequence stop: 669.
I. 793
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                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4749573"
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1 (Bases I to 671)

Xiu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,W., Gu,J., Chen,Z. and Han,G., Gu,W., Huang,W., Zhao,X., Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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Chinese National Human Genome Center at Shanghai
Sharional Human Genome Center at Shanghai
Shariona Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 CTACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCAGCA
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/mol_type="mRNA"
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This clone is available at CF
Location/Qualifiers
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/tissue_type="hepatocellular carcinoma, cell line"
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/clone lib="MIH MGC 100"
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ECRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/AnoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
GGCACGAG(G). Size-selected by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
Library."
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603613736F1 NIH_MGC_100 Homo sapiens CDNA clone IMAGE:5433632 5',
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      938
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLCM1909 row: g column: 09
High quality sequence stop: 714.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
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                                                                                                       GTCATGCATCTGTTGTTGCGGGGGGGGGGTGTCTCGTG----CCATGCTGCTGCGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

June 15, 2005, 12:22:30 ; Search time 159 Seconds (without alignments) 925.789 Million cell updates/sec

US-10-642-289-2 384 Title: Perfect score:

1 MDPAGGPRGVLPRPCRVLVL...........CVEPPPSWKPQQMPPPEEPL 384 OLIGO Gapop 60.0 , Gapext 60.0 Scoring table: Sequence:

1710399 segs, 383334425 residues Searched:

Total number of hits satisfying chosen parameters: Word size :

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2, Appli	Sequence 2, Appli	Sequence 26, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 21, Appl	Sequence 21, Appl	Sequence 21, Appl	Sequence 1, Appli	Sequence 2585, Ap	Sequence 3, Appli
SUMMARIES	ΩI	US-10-642-289-2	US-09-970-516-2	US-10-354-358-26	US-10-619-344-2	US-10-715-117-2	US-10-053-510-21	US-10-348-052-21	US-10-622-011-21	US-10-479-933-1	US-10-264-237-2585	US-09-796-487-3
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,	Query Match	100.0	87.5	87.5	87.5	86.7	83.3	83.3	83.3	74.7	74.2	65.1
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US-10-723-860-722 US-09-933-767-328 US-10-004-860-328 US-09-784-810A-2 US-09-784-810A-2 US-09-784-810A-2 US-09-933-767-788 US-10-004-860-788 US-10-004-860-788 US-10-642-289-13 US-09-796-487-5 US-09-796-487-5 US-09-796-487-5 US-09-796-487-1 US-09-796-487-1 US-09-796-487-1 US-09-796-487-1 US-09-796-487-1 US-09-796-487-1 US-09-796-487-1 US-09-796-487-1 US-09-796-487-1 US-09-796-487-1 US-10-642-289-12 US-10-642-289-12 US-10-642-289-12 US-10-642-289-12 US-10-642-289-12 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-642-289-11 US-10-631-958-3 US-10-631-958-3 US-10-631-958-3 US-10-425-115-2940 US-10-363-641-369-9	US-10-425-1115-35 US-10-425-1115-32 US-10-425-1115-32 US-10-282-122A-5 US-10-282-122A-5 US-10-925-301-135 US-10-925-301-135 US-10-928-10-20 US-10-622-011-29 US-10-348-052-20 US-10-622-011-29 US-10-348-052-20 US-10-348-052-20 US-10-348-052-10 US-10-348-052-10 US-10-348-059-16 US-10-004-860-78 US-10-004-860-78 US-10-004-860-78 US-10-425-115-36 US-10-425-115-36 US-10-425-115-36 US-10-425-115-36
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SEQ ID NO 2
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 2, Application US/10642289;
Publication No. US20040132053A1;
GENERAL INFORMATION:
APPLICANT: PITSON, Stuart M
APPLICANT: PITSON, Stuart M
APPLICANT: Pian, WATTENBERG W
APPLICANT: Pu, XIA
APPLICANT: MATHEW, VADAS A
ITILE REFERENCE: PATSON=1
CURRENT MATHEW, VADAS A
ITILE REFERENCE: PITSON=1
CURRENT MATHEW, VADAS A
ITILE REFERENCE: PITSON=1
CURRENT FILING DATE: 2003-08-18
PRIOR FILING DATE: 2003-08-18
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: PCT/AU00/00457
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PRIT
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Sequence 2, Application US/09970516
Patent No. US20020099029A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: polymucleotides encoding sphingosine kinases
FILE REPERENCE: 4.316.7
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
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181 SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
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                                                                            Length 384;
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                                                                            DB 16;
                                                                         Query Match 100.0%; Score 384; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches
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; ORGANISM: Homo sapiens
US-10-642-289-2
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US-09-970-516-2
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Sequence 2, Application US/10619344

Publication No. US20040086487A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REPRENCE: 4-31617

CURRENT APPLICATION NUMBER: US/10/619,344

CURRENT FILING DATE: 2003-07-14

PRIOR APPLICATION NUMBER: US/09/970,516

PRIOR APPLICATION NUMBER: US/09/970,516

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn version 3.1

SEQ ID NO S.
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87.5%; Score 336; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 336; Conservative 0; Mismatches
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; Sequence 2, Application US/10715117
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ORGANISM: Homo sapiens
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APPLICANT: Lightcap, Eric S.
APPLICANT: Lightcap, Eric S.
APPLICANT: Milliamon, Mark
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Publication No. US20030157082A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                              Hunter, John Joseph
MacBeth, Kyle J.
Tsai, Fong-Ying
Lesson, Andres
Lightcap, Eric S.
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Matches 336; Conservative
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; ORGANISM: Homo sapiens
US-10-354-358-26
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APPLICANT:
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; Sequence 21, Application US/10348052
; Publication No. US20030219782A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyrst, Henrik
; TITLE OF INVENTION: OCOMPOSITIONS AND METHODS FOR THE MODULATION
; TITLE OF INVENTION: OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
; FILE REFERENCE: 200116.405
; CURRENT APPLICATION NUMBER: US/10/348,052
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 1.9e-303;
iive 0; Mismatches 0;
      100.0%; Pred. No. 1.9e-303;
tive 0; Mismatches 0;
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                              Matches 320; Conservative
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Matches 320; Conservative
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ORGANISM: Homo sapiens
         Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Stylest, Henrik
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: MATHODS OF USE THEREFOR
FILE REPREMENCE: 200116,402C2
CURRENT APPLICATION NUMBER: US/10/053,510

CURRENT FILING DATE: 2002-01-17
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Best Local Similarity 100.0%; Pred. No. 4.2e-316;
Matches 333; Conservative 0; Mismatches 0; Indels
Publication No. US20040171037A1
GENERAL INFORMATION:
APPLICANT: L1, JING
APPLICANT: FOWERS, SCOTT
APPLICANT: SIN, WUN CHEY
APPLICANT: XANG, JIANXIN
TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
FILE REFERENCE: 38002-0062
CURRENT APPLICATION NUMBER: US/10/715,117
CURRENT FILING DATE: 2003-11-18
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/427,202 PRIOR FILING DATE: 2002-11-19 PRIOR APPLICATION NUMBER: 60/434,434 PRIOR FILING DATE: 2002-12-19
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-715-117-2
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LENGTH: 398
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LENGTH: 368
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RESULT 10
US-10-264-237-2585
SEQ ID NO 1
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APPLICANT: Wang, Lijun
APPLICANT: Wang, Lijun
APPLICANT: Wang, Lijun
APPLICANT: Wang, Lijun
APPLICANT: Gamble, Jennifer
APPLICANT: Bomble, Jennifer
APPLICANT: Pitson, Stuart
TITLE OF INVENTION: SPHINGOSINE KINASE INTERACTS WITH TRAF2 AND
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
FILE REPERENCE: 65063-410USPC
CURRENT APPLICATION NUMBER: 2003-12-05
PRIOR APPLICATION NUMBER: PCT/AU02/00710
PRIOR APPLICATION NUMBER: PCT/AU02/00710
PRIOR SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                          Sequence 21. 4. Application US/10622011
Publication No. US20040126834A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
TITLE OF INVENTION: OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
FILE REFERENCE: 200116.405C1
CURRENT FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match 83.3
Best Local Similarity 100.
Matches 320; Conservative
                                                                                                                                                                                                                                                                                                     LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-479-933-1
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; Sequence 2586, Application US/10264237
; Publication No. US20040009491A1
; GRENEAL INFORMATION:
    APPLICANT Birse et al.
    TITLE OF INVENTION:
    FILE REPERBNCE: PAL31P1
; CURRENT PAPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR PILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SEQ ID NO 2585
; LENGTH: 333
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                                                                                                                                                                                Length 384;
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                                                                                                                                                                                74.7%; Score 287; DB 17; L
100.0%; Pred. No. 3.4e-271;
tive 0; Mismatches 0;
                                                                                                                      ) OTHER INFORMATION: Xaa = Any Amino Acid
US-10-479-933-1
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Best Local Similarity 100.C
Matches 285; Conservative
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Best Local Similarity 100.
Matches 287; Conservative
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US-10-264-237-2585
LENGTH: 384
TYPE: PRT
ORGANISM: Homo sapiens
                                                          FEATURE:
NAME/KEY: VARIANT
LOCATION: 354
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Sequence 72. Application US/10723860

Sequence 72. Application No. US20040255606A1

GENERAL INFORMATION:
APPLICANT: AA12, Natesha

APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

FILE REFERENCE: 05882.0193.NPUS01

CURRENT APPLICATION NUMBER: 00/193.860

CURRENT PILING DATE: 2002-11-26

PRIOR APPLICATION NUMBER: 60/429,739

PRIOR PILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: Patentin Version 3.2
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100.0%; Pred. No. 4.6e-235;
tive 0; Mismatches 0;
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TITLE OF INVENTION: 207 Human Secreted Proteins FILE REFERENCE: P2007P2
CURRENT APPLICATION NUMBER: US/09/933,767
CURRENT FILING DATE: 2001-08-22
PRIOR PILING DATE: 2001-02-21
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PAPLICATION NUMBER: 60/193,170
PRIOR PILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: 09/205,258
PRIOR PILING DATE: 1998-12-04
PRIOR PLING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: 60/048,885
PRIOR PILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/048,885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 250; Conservative
241 LEEPVPSHWT 250
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-933-767-328
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| Sequence 3, Application US/09796487
| Sequence 3, Application US/09796487
| Sequence 3, Application US/09796487
| SEQUENCAL INFORMATION:
| TITLE OF INVERTION: Sphingosin Kinase, Cloning, Expression and Methods of Use |
| TITLE OF INVERTION: Sphingosin Kinase, Cloning, Expression and Methods of Use |
| TITLE OF INVERTION: Sphingosin Kinase, Cloning, Expression and Methods of Use |
| TITLE OF INVERTION: Sphingosin Kinase, CURRENT APPLICATION NUMBER: US 60/186,532 |
| PRIOR FILING DATE: 2000-03-03 |
| PRIOR FILING DATE: 2000-03-05 |
| PRIOR FILING DATE: 2000-05-05 |
| PRIOR FILING DATE: 2000 |
| DATHER INFORMATION: BARK SENTOR: (1) - (1344) |
| PRIOR FILING DATE: 2000 |
| DATHER SETTION NUMBER: AAF73423 |
| PRIOR FILING DATE: 2000 |
| DATHER SETTION NUMBER: AFF73423 |
| PRIOR ELECTRON NUMBER: AFF73423 |
| P
                                        61 RELVRSEELGRWDALVVWSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
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   GPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVR 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHYAGYEQVTNEDLLTUCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPANLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                            292 AGVSRAMLLRIFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKG 336
                                                                                                                                                                                     241 AGVSRAMLLRLFLAMBKGRHMEYECPYLVYVPVVAFRLEPKDGKG 285
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DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
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R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,875
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,374
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,917
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,949
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,949
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R APPLICATION NUMBER: 60/048,898

R PILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,962

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06
                                                                                                                                                                                                                                    R APPLICATION NUMBER: 60/048,884
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,884
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,971
R APPLICATION NUMBER: 60/048,971
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,964
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,964
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,882
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,899
R FILING DATE: 1997-06-06
                                                                  R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,880

R FILING DATE: 1997-06-06

R PILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,896
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
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APPLICATION WUMBER: 60/049,019
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/048,972
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
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APPLICATION NUMBER: 60/048,883
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,897
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APPLICATION NUMBER: 60/068,054
                                                                                                                                                                    FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,876
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,895
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APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,375
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,881
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; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-933-767-328
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; Publication No. US20030065160A1
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 328
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54.4%; Score 209; DB 10; L

Best Local Similarity 100.0%; Pred. No. 3.9e-195;

Matches 209; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/066,053
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR PLING DATE: 1997-12-18
PRIOR PELING DATE: 1997-12-18
PRIOR PELING DATE: 1998-01-30
PRIOR PRILING DATE: 1998-01-30
PRIOR PELING DATE: 1998-05-18
PRIOR PELING DATE: 1998-07-15
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US-10-004-860-328
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                                                                                                                                                         ; LOCATION: (36); COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-004-860-328
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
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CURRENT PELLING DATE: 2001-12-20
EARLIER APPLICATION NUMBER: US/205,258
EARLIER APPLICATION NUMBER: 09/205,258
EARLIER PLING DATE: 1998-12-04
EARLIER PLING DATE: 1998-06-04
EARLIER PELLING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,899
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APPLICATION NUMBER: 60/048,894
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 328, Application US/10023282
Publication No. US20030092893A1
GENERAL INFORMATION:
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                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                           NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-023-282-328
LENGTH: 293
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; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-023-282-328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPS 156
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; Pred. No. 3.9e-195;
0; Mismatches 0;
                                                            EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-0
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,901
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ORGANISM: Homo sapiens
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Best Local S:
Matches 209
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